

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTC**ATG**GCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCACTTGGCATTGTTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTTCGAACTGGTCGCTGCCATCGTAGG
ATTTGTTTTTCAGACATGAGATTAAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGTTGTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTTCCTTTGGAGTTGCTTGCTTCCAACCTGATTGGAATCTTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAGTATGAGATAGTG**TAA**CCCAATGTATCTGTGGGCCTATTCCTCT
CTACCTTTAAGGACATTTAGGGTCCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTTCATGTTAGATCG
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDIRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGT
GTTCCCTCTTTCCGGGGTCCCTACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTTCAGTTGTTAAAAACAAATAGGATGCAAATTCC
TCAACTCCAGGTTATGAAAACAGTACTTGGAACCTGAAAACCTACCTAAATGATCGTCTTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCCGCCACCAAGGAGGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
GGCAGTAATACGGAATCTTGTAAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
GAAAAGTGTTCTGCCCCGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
CCAAGCCTTGCTGCTCACAGGGCAAAGGAGAATATTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPFRGRGPHEPRRKKQNV DGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTCAGCCCATTGGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCCTAACGGACTG
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTCTTCCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCGCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA
AAAAAAAAAAAA

FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPPFYFHISM
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCAGATTTTAAAGCCCATTTCTGCAGTGGGAATTTTCATGAAGCTAGCAAGAGGACACCATCTT
CTTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAAATGCTCTTTTGGGT
GCTAGGCCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAG
ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC
AGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTA CTGTGCTTCTGGATGTGACCGACCCAG
AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT
CTGATCAATAATGCTGGTGTTCCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTTGGAGGTCGCCTTGCA
ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAAGGTTTCAATGACAGCTTAAG
ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAACAA
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA
GACATCAAACAACAATATGGAGAAGGTTACATTGAAAAAAGTCTAGACAACTGAAAGGCCAA
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTTCTGGATACCTCTG
TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
TCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTG
CTCAAGTTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCTGT
ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG
ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTT
AAGTATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406

><subunit 1 of 1, 319 aa, 1 stop

><MW: 35227, pI: 8.97, NX(S/T): 3

MLFWVLGLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT
 ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNOVGKGLWGLINNAGVPGVLAPTDW
 LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
 NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLD
 KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLKQK
 AELANPKAV

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

CCGCGGCTGTTGACGGCGCTGCG**ATG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
CCTCTCAGTCGGACTTCTGACGCCGCCAGTGGGCGGGGCCCTTGGGCCGTCGCCACCACT
GTAGTCATGTACCCACCGCCGCCGCCGCTCATCGGGACTTCATCTCGGTGACGCTGAG
CTTTGGCGAGAGCTATGACAAACAGCAAGAGTTGGCGGCGGCGCTCGTGCTGGAGGAAATGGA
AGCAACTGTTCGAGATTGCAGCGGAATATGATTCTCTTCTCCTTGCCTTTCTGCTTTTCTGT
GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAGCTCTGGCTTTCAGGCTAGAGGA
AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAACCAGCAAATCCACCCGCTCTTACCAG
CTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTTCGTCACAGAAAGACACA
AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA
TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCCTGTGGATCCCCGCCCGGAAGGAG
ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG
CTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG
CACACCAAGTGCATCTGAACATATCGCCAGAAGGGCGTGATTGACGTCTTCTGATGCATGGA
AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT
GAGTGGTTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT
GAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGGAAGAAGTTACACTTTGAAAAGGACG
TGGACGTCAACCTGTTTGAGAGCACGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTACCAC
CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGAAATCGGCTAATGCCTGC
CTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCAC
CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGG
GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA
CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG
GCCTCTTACCCACCTGGGCGTATTACAGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA
AGCCATCGAGGGTGTGAGAACGCACCTGCTGCGGCACTCCGAGCCCAGTAAGCTCACCTTTG
TGGGGGAGCTTGCCACCGGCCGCTTCAAGTGCACAGATGGACCACCTGGTGTGCTTCTGCCA
GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCCAGGA
GCTCATGGAGACTTGTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
TGCACTTCAACCTTTACCCCCAGCCGGGCCGTCGGGACGTGGAGGTCAAGCCAGCAGACAGG
CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTCACAGGGG
CCGCAAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCC
CTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCAGCCTAGGGAC
AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA
CCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCACCTCTGCCTATCT
GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG
CTGGGTCTGTGGCATTTTCCAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGCCCAGGCT
CTGAACTGGCTCTGGGCTCCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA
GGCCGTGAGTCTTGGTGTGATGCGGGGTGGGCTGGGCGGCTGGAGCCTCCGCCTGCTTCTC
CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA
GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCCAGGGTGCAGC
TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCCAATCCAAGGGTCTGGAGGGGGCTGCCGTGA
CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTC
CTGGCCGCCCCGCAGGGGGCTTGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCTC
CCAGTGGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTTGCTCTAACCGCAA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529

><subunit 1 of 1, 699 aa, 1 stop

><MW: 79553, pI: 7.83, NX(S/T): 0

MAACEGRRSGALGSSQSDFLTTPVGGAPWAVATTVVMPPPPPPHRDFISVTLSFGESYDN
 SKSWRRRSCWRKWKQLSRLQQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE
 IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
 KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSSRAEVPTKPPLPPARTQGTPVHLNY
 RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
 RKWVSKKLHFEKDVDVNLFESTITIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
 PYSDVNIGTGVAHPPRWTSDSTVAEVTISIQLFRELSTGDKKFQEAVEKVTQHIHGLSGK
 KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
 HLLRHSEPSKLTFFVGEAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
 MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPETVESLFYLYRVTGDRKYQDWG
 WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
 AYVFNTEAHPLPIWTPA

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

GGCGCCGCTAGGCCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC
CGCCTCTCCGCACGATGTTCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGGTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTGGC
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACC GCCTGGCAGTGCTGGT
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCTTGA
GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC
CGGGCAGCGCTCATCAACGTGGGCTTCTTGAGAGCAGCAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTGCGCGGC
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC
GCCCCTCGGGAATCACAACCTGGGTACAAGACATTTGCGCACCTGCATGACCCAGCCTGGCGG
AAGAGGGACCAGAAGCGCATCGCAGCTCAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC
CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC
AGCTGAGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
CAAGGCCTCAGGTCGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG
GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG
GGACCCCCCTGCCTTCTGCTCACCTACTCTGACCTCCTTCACGTGCCCAGGCTGTGGG
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCC
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AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVR
GQGQETSGPPRACPPEPPPEHWEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
CCTGTTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGT
AAATATGTCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
CCTGTTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGT
AAATATGTCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 14

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ
PRGEGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

14/249

FIGURE 15

GGGAGCCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCCAGCCGACGACAAAG
GAGCATGTCCGCGCCGGGGAAGGCCCGTCTCTCCGGCCGCCATAAAGCTCCGGTCGCCGCTGG
GCCGCGCCGCGCTCTGCCCCGCCGGGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCG
CTCGCCCCGCAGGCCCCGGCCCGCAGC**ATGG**AGGCCACCCGGACGCCGGCGGGGGCCGCGCGCA
GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGGCGGCG
GCGGCGGCGCCGCGGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCCGAGGGGCTGGC
AGGGCGGCGGGCGCCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAAGCTCGCGCAGGTCCT
GCCCCCAGATACTCTGCCCAACCGCACGGTCACCCTGATTCTGAGTAACAATAAGATATCCG
AGCTGAAGAATGGCTCATTTTTCTGGGTAAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT
CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCATCTCTAAAAAGATTGGATCT
GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTTCAGGACTCACCAATCTGGTTC
GGCTAAACCTTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTTGATTATCTTGCG
TCATTACGGTCTTTGGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGAT
GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGT
CACTGCAGGCCCAACCAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT
GAATTGCCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGAGACAGCCT
TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTTGTGGTATCAGGATG
GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGAACATGATTCACAAC
TGCTCCTTGATTGCAAGTGCCCTAACCATTCTAATATTAGGCTGGATCTACTGGAAATTG
GGGCTGTGATGTCCAGACCAAACGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG
AGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTGGTAAACAACAAGGTGACTTCAGATGG
CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG
GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGCGCGAGATGTGATAGAGGTGGCT
TTTGGGCAGATGATGATTATTCTCGCTGTGAGTATGCAAATGATGTCTACTAGAGTTCTTTAT
ATGTTTAATCAGATGCCCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC
TTACACTGTGGAAGCAGCCAACCTTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA
TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT
GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC
TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG
GAGCTCACGTTTATTCAACATATTCACCCAATATTGCTCTGGAAGCTTATGTCATCAAGTCT
ACTGGCTTCACGGGGATGACCTGTACCGTGTTCAGAAAAGTGGCAGCCTCTGATCGTACAGG
ACTTTGCGATTATGGGAGGCGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTTAAGT
GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT
AAGACTATTTACAGT**TAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA
AAAGATTTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAACCTA
ACCAGGAAGAAGTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCCTTTGATTCCCTTT
CTTCACATAAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAATATACT
ATTGTTACATGTGAAAAAATTTTATTTGACTTAAAAGTTTATTTATTTGTTTTTTTTGCTCCT
GATTTTAAGACAATAAGATGTTTTTCATGGGCCCCCTAAAAGTATCATGAGCCTTTGGCACTGC
GCCTGCCAAGCCTAGTGGAGAAGTCAACCCTGAGACCAGGTGTTTAAATCAAGCAAGCTGTAT
ATCAAAATTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTTTAAAAAAAGTATTTCA
TTGAAGCAAGCAAAATGAAAGCATTTTTTACTGATTTTTTAAATTTGGTGCTTTAGATATATTT
GACTACACTGTATTGAAGCAAATAGAGGAGGCACAACTCCAGCACCCCTAATGGAACCACATT
TTTTTCACTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTTAAATCTCACAG
TACTTTATTTCTGTCTTGTCCCTCAATAATATCACAAACAATATTCCAGTCATTTTAATGGC
TGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAATA
TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
VVCSSLELAQVLPPDTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT
EYLLCDCNIIWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPLELPSFYMTP
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT
ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLGIT
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNL
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
VFQKVAASDRTGLSDYGRDPEGNLDKQLSEKCNVSNTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560

FIGURE 17

GCGTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA
TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTTGGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

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FIGURE 19

CTGTCGTCTTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC
 CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCCCTCTGCTAAGACC
 GCTGCC**ATG**CCAGTGACGGTAACCCGCACCACCATCACAACCACCACGACGTCATCTTCGGG
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGCTTCTGCTTCTCCGTGACCCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCCTGCTATGCGGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCCTGTCCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCCCCGGCCCGGCGAG
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG
 CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG
 GAGTGCACCAACGTGCTACCCATCCCCTTCCCCAGCTTCCTGTGCGGGCTGGCCTTGCTGTC
 TGTCTCCTCTATGCCACCGCCCTTGTTCTCTGGCCCTCTACCAGTTCGATGAGAAGTATG
 GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGT
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGCACCTCTGCCACCTGGTTTTTGTCAAGGT**CTAAG**ACTCTCCCAAGAGGCTCC
 CGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTTCTTTATGGAGTACTTCTTTCC
 TCCGCCTTTCTCTGTTTTCTCTTCTGCTCTCCCTCCCTCCACCTTTTTCTTTCTTTCC
 CAATTCCTTGCACTCTAACCAGTTCCTTGGATGCATCTTCTTCCCTTCCCTTTCTCTTGCTGT
 TTCCTTCTGTGTTGTTTGTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT
 CTTTTCTTTCTTTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTTCAAGCGATTCTCCTCC
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTTGCCTGTCGGCTTCTTATCTGCCTGT
 TTTGCAAGCACCTTCTCCTGTGTCCTTGGGAGCCCTGAGACTTCTTTCTCTCCTTGCCCTCA
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGAGCCGTCCATGCCACAGCCCC
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTGTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT
 CCCAGTGGAGGAAGGTGTGAGTGTACTTCCCCTTTAAATTAAAAACATATATATATATAT
 ATTTGGAGGTCAAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCCTGGGTCCCTAGG
 CCCCGCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT
 CTGTGGTATGAAAAAG

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTY
VQFLSHGRSRDHAI AATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQP ALEWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

[illegible]

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKVMHMDPNYCHPSTSLHLCS
 LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSLEDGLLGSPARLASQLLGDE
 LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
 QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
 285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCT
 GGCACCTCCTGCTCAGTGCGACATTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGA
 CAGATTCTTTTTCAGACAGGACAACCTGTGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAG
 CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
 TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG
 AAGCCTACA**ATG**TTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCT
 ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACACAGAACATTGCAGAAGTTT
 TTAACAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTTAACTCAGATAAA
 GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCTCCTTTGAATCTACCCAACAA
 CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCAGTCTAA
 AACCCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT
 TGGAAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
 TGCTCTGTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTGATA
 ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCCCTTG
 ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
 TCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTCACCAATAATTCAAACTCTTTCCAA
 ATACGTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT
 GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAAAAGGAAAAC
 GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAAGTTCTGCGATTAGACA
 ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTGAAT
 GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTTCCTATGGATGACATACC
 TCCACTTCGTACTTCTGTAT**TAGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA
 CATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT
 TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
 CCAAAGGTTTTCTTTCTTACAATTTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT
 TGTATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT
 TCACCATTACAGCCCTGCCTCATAACTAAATAAAAAATTATTCACCAAAAAATTCTAAA
 ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
 TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
 GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
 TAGTACGTTATAATTTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA
 CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT
 TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTCTTAATATATCTTAGGCTTCAA
 TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSNFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTNNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNTPSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNSA
MPESEENARDGIPMDDIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACT**ATG**GTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT
 TCATGCCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGCAG
 CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAAGTGC
 TATCTGATGCCCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGG
 CAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
 AAGTCCTTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
 AAAAAAGGAAAAAAAAAAAAAACTACTAACCAGTCAAGCTCTTGTCAAATTTTAGTTTAAT
 TGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTTCTTTGCATTTATAG
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCC
 GTTGTTTTTTTTGTTTGTGTTTTTTTTCTTTTCCTTTAAGTAAGCTCTTTATTCATCTTATG
 GTGGAGCAATTTTAAAATTTGAAATATTTTAAATTGTTTTTGAACTTTTTGTGTAAATATA
 TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTTTCATTTTGTACAACTTTCTTGAATTTAGA
 AATTACATCTTTGCAGTCTGTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
 TTCATGAGACAGTCATTTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAA
 CCCTATAATAAATTTTACTCTATACAAAAAAAAAAAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIIRDVSNLGIIFIYQLCNNRKSFRLRRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT
 CTTCCAGCCCAGGTGCCCCCACTCTCGTCCATTCGGCGGGAGCACCCAGTCCTGTACGCC
 AAGGAACTGGTCCTGGGGGCACCATGGTTTCGGCGGCAGCCCCCAGCCTCCTCATCCTTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
 CGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCCTGGGG
 GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA
 TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC
 GTGGACCAGAGTGACCGGGCCGGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG
 CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA
 GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCCTTG
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCAG
 GAAGCCCAGGGACCAGTGGGTCCCCCGAAAGCCCCTGTGCTTGACAGCAGTGTCCACCCAG
 TGTCTAAAGTCCTCCCGGGCTGCCAGCCCTGACTGTGCGGGCCCCCAAGTGGTCACCTCCCC
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGGCCTCCCTGTGG
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA
 GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
 ACAGCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACCTACTTTTTTAAACA
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCCTGAAGG
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC
 TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGAACCTTCTCCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTTGAGGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG
 TGTCCACAATATTCGTCAGTCCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCACAATAAACCTTTATTCCGGCCTGAAAAAAAAAA
 AAAGA

FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLLLLLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
QGGELEGSLLLLAQEAQGPVGPPEPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

[illegible]

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
```

```
><subunit 1 of 1, 440 aa, 1 stop
```

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEG VGKAI GKEAGGA
 AGSKVSEALGQGTREAVGTGVRQVPVGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
 ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGGQGNPGGLGTPWVHGYPGNSAGSFGM
 NPQGAPWQGQGNNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
 GSQSGSSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGNSGSGSRGDSGSESSW
 GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
 GSGSDNYRGQGS SWGSGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
 RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCCGGGCGGTGCTCACCG
 TGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGGACATCTTCA
 CTCTCCTGCTGCGCCTGCACCGGAGCTTGGTGTGTGCGAGGAGAGTGAGGGGAAGATGTGTTTCTGAACAAGC
 TGCTGCTACTTGCTGTCTGGGCTGGCTTTTCCAGATTCCCACAGTCCCTGAGGACTTGTTCTTTCTGGAAGAGG
 GTCCCTCATATGCCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCGCCTGTGGTGGACCAGC
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAAGTGTGCTCGCTTCGTGGGTGTGAGGCAGTAGTG
 GACGGAGTGGGGGCTTCATGAGGAAAATCACCCCCACCACTACCACCAGCCTGGGAGCCCAGCCTTCCCAGACCA
 GCCAGGGGCTGCAGGCACAGCTCGCCAGGCCCTTTTCCACAACCAGCCGCCCTCCTTGCGCCGGACCGTAGAGT
 TCGTGGCAGAAAGAATTGGATCAAACCTGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGGCCAGG
 CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGACCCAGCCAGCTGTTGGAGATCT
 TGTGTTCCAGCTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG
 GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGCAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC
 TTGCAACAGAGAAAGCCTGTGCTTGGCTGTGAGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG
 TGAGTCGCACACTTCGAGCCCAGGTCCTGAACCTGCTGCCCCGGGGGAGCGGAGGGGCTGCTCCCGCGCTTGA
 GTGCTCTCCTTGGCCGTGGGGCCACGGGACCCTGACGAGGGAGTCTCCCCAGAGCATCTGGAACAGCTCCTAGGC
 CAGCTGGGCCAGACGCTGCGGTGCCGCCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTGCTCTGTG
 GAGTTAGCTTCCCTCCTCGTTGCAGATCAAATTCCTATCCTAGGGCCCCCGGCACAGTACAGGCTGGAGAGAGGG
 CAGGCTCGAAGGCTTCTGCACATGCTGCTTTCCTTGTGGAAGGAAGACTTTCAGGGGCGCGTTCCGCTGCAGCTG
 CTGCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGCTGCTATTCTTGCTA
 CGGGAGCTGGTGGAGAAGGCTGATGGGACGGATGGAGATAGAGGCCTGCCTGGGCAGCCTCCACCAGGCCAG
 TGGCCAGGGGACTTGTGCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGCCCCACCTGCCAGAACCC
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC
 CTGCCCTGGGCATTGCACCAGAACCCTGGACCCCCGCTCACGAGGAGGCCCAAGTGCCCAATGCAGACCCTCAC
 TGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTCACTGCCTGGCATCCACCACGCGA
 ATCCTAGAGGAAGGAGAGTTGGCCTGATTTGGGATTATGGCAGAAAAGTCCAGAGATGCCAGTCCCTGGAGTAGAA
 GAGGTGGTGTGTTGTTATCTCTTGGATACTAAATGAAATGAGGTGTGTGGGCTTGTCAACACAGAATCAAGCCT
 CATTTGCTATCCCAGCATCTCTAAACCTTTGTAGTCTTGGAAATTCATGACAGAGGCAAATGACTCCTGCTTAA
 TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT
 ATAAATGCCTAACACAGGCCGGGTCTGGTGGCTCATGCCTGTAATCCCAGCACTTTGAGAGGCCTGAGGTGCGCG
 GACTGCCTGAGGTGAGGAATTAAGACCAGCCTGGCCAACATGGCAAAACCCCATCTCTACTAAAAATAAAAAA
 TTATAGCTGGGCATGGTGGTGTGTGCCTGTAATCCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC
 CTGGAGGTGGAGGTTGCAGTGAGCCGAGGTCGCACCACTGCACTCCAGTCTGGGTAACAGAGCGAGACTTTCTAG
 AAAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCCCTGTACCTTCAGCCCCG
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCATTAGAGCTTTTATAGAAATAA
 CTGGTTTTCTTTAAAAAAGGGCTTTTATTAAATTTCTCCCCACACGATGGCTCCTGCAATCTGCCACAGCTC
 TTTTCTTTTCTTTTAAAAAGGGCTTTTATTAAATTTCTCCCCACACGATGGCTCCTGCAATCTGCCACAGCTC
 TGGGGCGTGTCTGTAGGGAAGGCCCTGTTTCCCTGAGGCGGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTG
 GCCGTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTCTTGGCGGCACAGAGCTGCGGGGTCTGGGGGCACCGGG
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCTGTCTCTTAACCGACACCCTGAGGTGCTCCTGAGATGCTG
 GGTCCACCCTGAGTGGCACGGGGAGCAGCTGTGGCCGGTGTCTCTCYTAGGCCAGTCTGGGGAACTAAGCTC
 GGGCCCTTCTTTGCAAAGACCGAGGATGGGGTGGGTGTGGGGGACTCATGGGAATGGCCTGAGGAGCTACGTGT
 GAAGAGGGCGCCGGTTTGTGGCTGCAGCGGCCTGGAGCGCCTCTCTCCTGAGCCTCAGTTTCCCTTTCCGTCTA
 ATGAAGAACATGCCGTCTCGGTGTCTCAGGGCTATTAGGACTTGCCCTCAGGAAGTGGCCTTGGACGAGCGTCAT
 GTTATTTTCACAACTGTCTGCGACGTTGGCCTGGGCACGTGGAATGGCCCATGTCCCTCTGCTGCGTGGAC
 GTGCGGTGCGGAGTGCGCAGCCAGAGGCGGGGCCAGACGTGCGCCTGGGGGTGAGGGGAGGCGCCCCGGGAGGG
 CCTCACAGGAAGTTGGGCTCCCGCACCACCAGGCAGGGCGGGCTCCCGCCGCCGCCGCCACCACCGTCCAGG
 GGCCGGTAGACAAAGTGAAGTGCAGCTTGGGCTGCTGCGCAGCAGGTAGCCCTTGATGCAGTGGCGCAGCGCG
 TCGTCCGCCAGCTGGAAGCAGCGCCCTCCACCAGCACGAACAGCCGGTGGCCT

FIGURE 32

MCFLNKL L L L L L A V L G W L F Q I P T V P E D L F F L E E G P S Y A F E V D T V A P E H G L D N A P V V D Q Q L L Y T C
C P Y I G E L R K L L A S W V S G S S G R S G G F M R K I T P T T T T S L G A Q P S Q T S Q G L Q A Q L A Q A F F H N Q P P
S L R R T V E F V A E R I G S N C V K H I K A T L V A D L V R Q A E S L L Q E Q L V T Q G E E G G D P A Q L L E I L C S Q L
C P H G A Q A L A L G R E F C Q R K S P G A V R A L L P E E T P A A V L S S A E N I A V G L A T E K A C A W L S A N I T A L
I R R E V K A A V S R T L R A Q G P E P A A R G E R R G C S R A

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
 AAGACTCTCTGCTTTTGCCACAGCAGTTCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**
 AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA
 GCCGCCGACCTGTCAACCTCAAGAAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
 AACAAGACACTGCCCTCTCGGTGCCACCAAGTGTGTGATTGTGAGCAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCGTGGCCCATTC
 AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT
 CATCTTCTGGGGGCCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGTGTGATCC
 AGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCCGGCCGCATGCGG
 CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCTGTTGTT
 GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG
 GCATGGTCCCCCCCCAACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCCAAGGGGCCGGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG
 CAACCACCACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGCCCAGCTGTATGGCA
 TCACCTTCTCCCACCCCTCCTGGACC**TAG**GCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
 AGGAGAAGCAGCCTCCGCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
 TGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTTCTGAGTCAATCTG
 AGGCTAAGGACATGTCCTTTCCCATGAGGCCTTGGTTCAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTGGTGTTG
 CCCCCTCAATTTCCAGCACCAGAAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAATTTGTGGGGTGTGGAGGTTGTGGGGGCGGTGGGGAGGTCCAGAGGTGGGA
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCTTCCCCCTCTCTGGG
 CACCCTTCTGCCCACACCAGTTTCCAGTGCGGAGTCTGAGACCCTTTCCACCTCCCCTACAA
 GTGCCCTCGGGTCTGTCTCTCCCGTCTGGACCCTCCAGCCACTATCCCTTGCTGGAAGGCT
 CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTAGGGTATTTTTC
 GCAAACCTCCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT
 TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCT
 CTAGCAGGGAGGTTTTCCAACCTGTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA
 CTGGGGGCTTCCGAGGGTCTCCCTCGACCCTCTGTCTGCTGGGATGGCTGTGCGGAGCTGT
 ATCACCTGGGTTCTGTCCCTGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCCTCAGTGG
 GGTGTGTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG
 GGGCGGTGACTGCCCCAGACTTGGTTTTGTAAATGATTTGTACAGGAATAAACACACCTACGC
 TCCGGAAA

FIGURE 34

MSSNKEQRSAVFVILFALITILILYSSNSANEVFHYGSLRGRSRPVNLKKWSITDGYVPIL
GNKTLPSRCHQCIVIVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
SSVFRVLRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIARELCHVHVYGMVPPNYCSQRPRQLQMPYH
YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

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GTTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCGCTT
 GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGTGTCTGAGGGGCTGG
 GGCAAAGGTGAAAGAGTTTTCAGAAACAAGCTTCTGGAACCCATGACCCATGAAGTCTTGTGACATTTATACCGT
 CTGAGGGTAGCAGCTCGAAACTAGAAGAAGTGGAGTGTGGCCAGGGACGGCAGTATCTCTTTGTGTGACCCTGGC
 GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACC**ATG**CTGCGTGGGACGATGACGGCGTGGAGAGGAATG
 AGGCCTGAGGTCACACTGGCTTGCCCTCCTCCTGACACTAGCACAGGCTGCTTTGCTGACTTGAACGAGGTCCTCAG
 GTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCCGGAGGCACTGTGATCTTGGGCTGCGTGGTGGAACTCCA
 AGGATGAATGTAACCTGGCGCCTGAATGGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCATCACC
 CACGGGACCCCTCGTCATCACTGCCCTTAACAACCACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCCTGCG
 GGGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCCAGCAGTG
 ATTGAAGTGGATGAGGGAACACAGCAGTCATTGCCTGCCACCTGCCTGAGAGCCACCCCAAAGCCCAGGTCCGG
 TACAGCGTCAAACAAGAGTGGCTGGAGGCCTCCAGAGGTAACCTGATCATGCCCTCAGGGAACCTCCAGATT
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAACCC
 TCCGGCTCCAGCGACAGGTCAGTGTGCGCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCGAGGCGCC
 CAAACCATCATCGTACCAAAGGCCAGAGTCTCATTCTGGAGTGTGTGGCCAGTGGAATCCCACCCCCACGGGTC
 ACCTGGGCGAAGGATGGGTCCAGTGTACCCGGCTACAACAAGACGCGCTTCCTGCTGAGCAACCTCCTCATCGAC
 ACCACGAGCGAGGAGGACTCAGGCACCTACCGCTGCATGGCCGACAATGGGGTTGGGCAGCCCGGGGCGAGCGGT
 ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTCACTTGGAGCTATCCAGCTGGTTCATCCCTGGGGC
 CAGAGTGCCAAAGCTTACCTGTGAGGTGCGTGGGAACCCCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCC
 CTCATCTCCAGCCAGCGCCTCCGGCTCTCCCGCAGGGGCCCTGCGCGTGTCTCAGCATGGGGCCTGAGGACGAAGGC
 GTCTACCAGTGCATGGCCGAGAACGAGGTTGGGAGCGCCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC
 ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCAGCAGCTCCTGTATCACCTCCAACCTCGGCAAC
 CCTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCCAGACCCCCAACGTGAGTGGGGCCTGCTTCCCCGAAGTGT
 CCAGGAGAGAAGGGGCGAGGGGCTCCCGCCGAGGCTCCCATCATCCTCAGCTCGCCCCGCACCTCCAAGACAGAC
 TCATATGAAGTGGTGTGGCGGCTCGGCATGAGGGCAGTGGCCGGGCGCCAATCCTCTACTATGTGGTGAACAC
 CGCAAGTCAGGTCACAAATTCCTGTGACGATGGACCATCTGAGCATTCCAGCCAACAGCAGCCGCTGACCTC
 ACCAGACTTGACCCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACGTGTGCGGGAGAGGGCCAGACAGCC
 ATGGTCACTTCCGAAGTGGACGGCGGCCCCAACCCGAGATCATGGCCAGCAAAGAGCAGCAGATCCAGAGAGAC
 GACCTTGGAGCCAGTCCCCAGAGCAGCAGCCAGCCAGACCAGCGCCGCTCTCCCCCCCAGAAGCTCCCCGACAGG
 CCCACCATCTCCACGGCCTCCGAGACCTCAGTGTGACCTGAGCCATCTGAGCATTCCAGCCAACAGCAGCCGCTGACCTC
 CAGTCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCAGCGCCATCCCCCA
 TCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCTCCTACAAGTTTCGAGTCCGGGCTCTGAACATG
 CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGGGCTACAGCGGTGCGGTGTACGAGAGG
 CCGTGGCAGGTCTTATATCACCTTACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGGATCCATC
 CCAGCAAGTAACAACAACACCCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTGACAATGATAGT
 GACTACAAGAAGGATATGGTGGAAAGGGGACAAGTACTGGCACTCCATCAGCCACCTGCAGCCAGAGACCTCCTAC
 GACATTAAGATGCAGTGCTTCAATGAAGGAGGGGAGAGCGAGTTGAGCAACGTGATGATCTGTGAGACCAAAGCT
 CGGAAGTCTTCTGGCCAGCCTGGTTCGACTGCCACCCCAACTCTGGCCCCACCACAGCCGCCCCCTTCTGAAACC
 ATAGAGCGGCGGTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGCGGGTCTGTC
 CTGGGCTCCATCGTTCTCATCATCGTCACTTTCATCCCCCTTCTGCTTGTGGAGGGCCTGGTCTAAGCAAAAACAT
 ACAACAGACCTGGGTTTTCTCGAAGTGGCCTTCCACCTCCTGCCCCGATATGTTGGTGGCATTGGGAGGACTC
 CCAGGCCACCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
 AATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTACCCGGGCATGAAGCCCCAGCAGCACTGCCAGGCGAGCTTCAG
 CAGCAGAGTGACACCAGCAGCCTGCTGAGGCAGACCCATCTTGGCAATGGATATGACCCCCAAAGTCACCAGATC
 ACGAGGGGTCCCAAGTCTAGCCCGGACGAGGGCTCTTTCTTATACACTGCCCCGACGACTCCACTCACCAGCTG
 CTGCAGCCCCATCAGCACTGCTGCCAACGCCAGGAGCAGCCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGCC
 CCCGACAGTCTGTCTGGAAGCAGTGTGGGACCCTCCATTTCACTCAGGGCCCCCATGCTGCTTGGGCTTGTG
 CCAGTTGAAGAGGTGGACAGTCTGACTCCTGCCAAGTGAAGTGGAGGAGACTGGTGTCCCCAGCACCCCGTAGGG
 GCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCGGGGCCACTGGTGCCTGTGCTTTTGAACACCACCT
 CTCACAATTT**TAG**GCAGAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAAAGAAAA
 AGAGACAGAGAAAATTGGTATTTATTTTCTATTATAGCCATATTTATATATTTATGCACCTGTAAATAAATGTA
 TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTACCCGTTGAGGTTGGAGAGGGAAATAAAGAAGCTGCCA
 CCTAACAGGAGTCACCCAGGAAGACACCGCACAGGCTGGCGGGGACAGACTCCTAACCTGGGGCTCTGCAGTG
 GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTCATCACGAGCA
 TGAGGGAACAGCAAGGGGCACGGTATCACAGCCTGGAGACACCCACACAGATGGCTGGATCCGGTGTACGGGAA
 ACATTTTCTAAGATGCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAACCACTTCCAGAAAT
 CAATAATCCGTGGCAACATATCTCTGTAAAAACAAACACTGTAACCTCTAAATAAATGTTTAGTCTTCCCTGTAAAA

FIGURE 36

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTVILGCVVEPP
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARIIPPEAQTIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSOLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQMAENEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEGQGAPAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFTTGRPKPEIMASKEQQIQRDDPGASPOSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRNGGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMIIPASNNNT
 PIHGFYIYYRPTSDNDSDYKKDMVEGDKYWHSISHLQPETSIDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPLYLVGVVLSIVL
 IIVTFIPFCLWRAWKQKHTTDLGFPRALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCPSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTLPPDDSTHQLLQPHHDCCQRQEQAAGVQSGVRRAPDSPVLEAVWDPPFHSG
 PPCCCLGLVPVEEVDS PDSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC
CCAGGCTCCCGCGGGCCGACCCCGCGCAAC**ATG**CAGCCCACGGGCGCGAGGGTTCCCGCGC
GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCCC
AGCCTCTTCACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCCAGGCCTCACTACGCCAGG
CACCCCCAAAACCCTGGACCTTCGGGGTTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACCTCG
TGGACGGCCACAATGACCTGCCCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
GTAAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
GGGTGCCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCCTACTCTGAACTCGAGCTT
GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTTGGCGTGNAGGG
TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACAC
CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCTCTGG
AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG
TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAAATTATGACGGGACT
GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT
GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT
TCAGACAAGTGGAAAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
CCATATGGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCCCTCAGAAATGGACACCAGGC
TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCCTCAAATGCCT
CCCCATACCTTGTTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTC
TGCT**TGA**CACAGTCGGTCCCCGCAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
AGTTCATTACAAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

FIGURE 38

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817

><subunit 1 of 1, 487 aa, 1 stop, 2 unknown

><MW: 53569.32, pI: 7.68, NX(S/T): 5

MQPTGREGSRALSRRYLRLRLLLLLLLLLLRLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVRRESRAQSPVEAEFPYGQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPFTQWLC

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGC**CATG**
AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGCTGGTGCCCCAGCTGAAGCCAACAA
GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
GTGCCTGGCCATGACGTGGAGGCCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
CACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACTGAGCAA
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC
AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAGAT**GGGCTGG
TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAAGCCTGTGGCATTTCCTCCTT
CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGA
ATGGAGACATTGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGAAGATAAAGCTGGGTCTTCA
GGAATCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTGAGCATGTGTTCTTTCTGCAGTG
GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACCTGGA
AGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
CTGCTGCCGGTCCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC
CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
CACCACAGCCCCTGTACTTGGGTGCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGA
GAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAATTG
TTTTATTTCTCTCA

FIGURE 40

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPBGHDVEAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCGCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAA
GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGCCAACATCACGTTTTTAAAAATTGATT
TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA
TAGCTGCATTTATTTAGTCAGTTTTCATTGTCATAGTAATATTTTCATGTAGTATTTTCTAAG
TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATGTGTTTTTAAAGCCTTGGGCAGAAATTCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT
TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA
TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACCTACTACTTCTTGGGACCTCAAGCC
CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCTCTCT
CCTGGTTTTGGAGTCCTTTCTCTCCAGGCCAAAACCTTCGAGAATCAACACCTGGAGACAGTCC
CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAATATCTCTGTGTCTG
TCCACCAGCCACAGCCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG
ATCCCAGCTTCTGCAGTGGAAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT
TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
AAAATAGTAATCAGATTCCCATCAGCTTGTATTCTGAAGTCTTTAAGTGAGCCTTTGAATACA
TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTTCCGTCATTACCTCCTG
CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCCTCTTATGACC
AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
GGAACCATCATGAATGGACATGGTGGTGGTCTGAAGTCAGCAGACACTAGACAGTAAGTATAG
CAGCAAGCTACTCTTGTCTATGGCTGGTGCCAACCAAACAGAGGAAGAGGATAGCTCACGTGA
TGTGGAAAACACCAGTTGGTCAATGGCTCATTTCGT**TAA**AAAGCAGCCCTTTTGCTTTTTTTGT
TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATAACAGTATGCAT
TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCCATAAATCCCAGTGCTTTGGGGGGCC
AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAAACTC
TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCCG
CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
GTCTGAAAAGA

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTCACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCCGGG
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA
 CGGGCCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCACGC
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCACG
 ACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTCATCGTCCCCGAGAGCCGAGCCCAC
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC
 TGTCTCCTGGCCGCCCCGAGGCGCCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTAACTTGGCGGAGTTGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAAT
 GCAAA**TAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCTCCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAACC
 AAAATCCCACTGATGCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCTG
 AAGACATTCCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAACCTGGGGTCAGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCCTGGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTTAAAAAAAAA
 AAAAA

FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQV VHWDRQPPGVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEP PPRGSPGNGSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDLDKGFRKENCK

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 48

MAVVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYYIIFSLGI
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSWTRGFFAVTIVCMVILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGly
LLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF
CVTYVFFITS LIYPVAVCTNIESLNKGSGLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPLEFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

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FIGURE 50

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRI
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPKLGALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGGFFYLSFAEALR
AHSCLSDRLLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPARNL
KVLKADVLLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAAGTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT
GGACGCTCTGAAGCCACCCTGTCTCTGGAGGAACACGAGCGAGGGAAGAAGGACAGGGACTCGTGTGGCAGGAA
GAACTCAGAGCCGGGAAGCCCCATTCACTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCCCT
GCTGCTGTTCAAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCCACTTCCGACCCCGGCGTTGATCTGCAT
CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCGTCTTACCTCTTCTTGACCTGAA
CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGGTTTTCCAGAAGAACAATGACCTAACAAAGTTGCTG
CTTCTCAGATGCCAAGACTATGTATGAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGG
ATATAGAAAACCAACCAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTT
CTGTCTCTTGCAATAAGGTTATAAATCATCACCAGACAGTTTGTGCGCATCTTTGCTCAGAATAGGCCAGAGTG
GATCATCTCCGAATTGGCTTGTTACACGTAATCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC
CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGCTGAT
AGGGAATGTAGAGAAAGGCTTACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGATGATGACCTGAA
GCAAAGAGGGGAGAAGAGTGAATTGAGATCTTATCCCTATATGATGCTGAGAACCCTAGGCCAAAGAGCACTTCAG
AAAACCTGTGCCTCCTAGCCCAGAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAGG
AGCCATGATAACCCATCAAAATATTGTTTTCAAATGCTGCTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGCC
CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAGAGGATTGTACAGGCTGTTGTGTA
CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGTTTGGCTGGCTGACGACATGAAGACTTTGAAGCC
CACATTGTTTTCCGCGGTGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCCTT
GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
TTTTCTGGGACAAGCTCATCTTTGCAAGATCCAGGACAGCCTGGGCGGAAGGGTTCGTGTAATTGTCACTGGAGC
TGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTCAAGGTGTATGAAGCTTATGGTCA
AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAGGTACGTTGGGGTGCCCTGGC
TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAAGTACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT
CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACAGGAAGCCCTGGACAGTGTGGCTG
GCTTCACACAGGAGACATTGGTCTGGCTCCCGAATGGAACCTCTGAAGATCATCGACCCGTAAAAAGAACATTTT
CAAGCTGGCCCAAGGAGAATACATTGCACCAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCAGTGTACA
AATTTTTGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCCTGACACAGATGTACTTCCCTC
ATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT
AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTTAAACCTTTTGAACAGGTCAAAGCCATTTTCTTCATCC
AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACTT
TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATAGGATAAGGTACTTAAGTACCTGCCGGCCCACTG
TGCACTGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATTTGTTTTGCCTTTCTCCTATTTTTTTTAAACC
TGTTAAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACATATAATGTGTAAACTTAGTTCCCAAATAAATCA
ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA
GATCCCAGTTTATGTTCTGTGTCCTTCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT
CAAAGGGACCCTCTGTGCCTTCTTCTTTGTTTTGTGATAAACATAACTTGCCAACAGTCTCTATGCTTATTTACA
TCTTCTACTGTTCAAACCTAAGAGATTTTTAAATTTCTGAAAACTGCTTACAATTCATGTTTTCTAGCCACTCCAC
AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT
CTGCGTAAATTAATTTGTGTACTGAAGGGAAAAGTTTGATCATACCAAAACATTTCTTAAACTCTCTAGTTAGATA
TCTGACTTGGGAGTATTAATAATTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGCATTATTTA
CAGTAGGAAGTGGGGAGTAAATCTGTTCCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA
GGTGGGCCCAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCTCCTGAACTGGGAACAAAGATCT
ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTCTGTGAAGGAACCAACTGATCTCCCCACCCTTGATT
AGAGTTCCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAATGTAAAGTCTTTAAATAAAC
TATTACAGATAAAAAA

FIGURE 52

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFKLLFTKMLFI
 FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPPLDLNNQSVGIEGGARKGVSQKNNDLTS
 CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
 PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
 VLIGNVEKGFTPSLKVIIIMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
 LSVICFTSGTTGDPKGAMITHQNIVSNAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQ
 AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPVPRLLNRIYDKVQNEAKTPLKKFLLKLA
 VSSKFKEQLQGIIRHDSFWDKLIFAKIQDSLGGRRVIVTGAAPMSTSVMTFFRAAMGCQVY
 EAYGQTECTGGCTFTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
 GYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIKFKAQGEYIAPEKIENIYNR
 SQPVLQIFVHGESLRSSLVGVVVPDTPDLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
 GKESGLKTFEQVKAIFLHPEPFESIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

Important features:

Type II transmembrane domain:

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGCGCCGGCGGAGCGGCGGAGCAGTGAAGGGCCCTAGCGGGGCCCCGAGCGGGG
CCCCGGGGCCCCCTAAGCCATTCTCTGAAGTCACTGGGCTGGCCAGGACATTGGTGACCCGCCAAT
CCGGT**ATGG**ACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG
AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
GACAGGGGGCCGTGCTTTTCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCCTGGACA
CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
CTAGGCCGCCTGGAGCCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTGGACGTAGA
GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGTCTGGAGGATG
AGGCCCGGGAGCAGGGCCGGGGCATCCATGTCAATTGTCTCAACCAGGCCACGGGCCACGTG
ATGGCAAACGTGTGTTTTGACAGCTACTCACCTCATGAGGATGAGGCCATGGTGTCTATTCTT
CAACATGGTAGCGCCCGGGCAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC
TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC
TGGAGGGACACATGGGCCTTCTGTTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATT
TAAGTCACCTGCCCTCTCTTCTGGGGGACCCAGTCTGTGAAGACAGATGTGCCATTGA
GCTCAGCAGAAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC
TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA
GTTTACGCCCTGACCCACTCCCAGACAACAAGGTCTCAATGTGCCTGTGGCTGTCAATTGCAG
GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCCAGGGGGTGTCT
CCTCAGATGATAACAGTTTTTCAATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGC
ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTTCCGGAGGCCAAGTTTGTCTGTGGTT
CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTTCAGTTTTCTGAGCCAATCCATCCACCT
ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA
CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC
AGGAGGTCTTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGA
TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGATCATCCCTGACG
TTTCCCGATCCTACCACTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTACGAGGCC
TACTTCAAGAAGCACAAAGTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT
GAAGAAAGAAGCTTATGAAGTGAAGTTTACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
ACAGCAAGAACCCTTGTGAAGACTCTTCTCCTGCCAGACACAGAGGGCCACACCTACGTGGCC
TTTATTTCGAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAGTGCCCTCA
TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCCTGTGGAGATTGTTTCGGAAGAAGA
ACCACTTCTTGGTGGTGGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC
ACCCCAATTTTCTGGAGCCACCCCCAAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC
ATGAGACCTCCTCCAGGACCCTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT
TCCCTCCATCCTGTAGGATTTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTTTAACA
TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCCTGCTCCAACACCCCGTTCTGAGTT
AAAAGTCTATTTATTTACTTCCTTGTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG
ATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCACTTTCCAGGCCTGGCTCAGAATCTA
ACCTATTTATTGACTGTCTGAGGGCCTTGAAAACAGGGCCGAACCTGGAGGGCCTGGATTTC
TTTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC
CAACCCATGGACAGGCCCAGCTGGGGCCCATGCTGACACAGACTCACTCAGAGACCCTTA
GACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGATTTCCAAAGCTGGATAAGTT
GGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185

><subunit 1 of 1, 660 aa, 1 stop

><MW: 75220, pI: 6.76, NX(S/T): 0

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVEDTYSPEHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEPMDDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRSLYKEELEPKWPTPEKLWDWDMWMMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLKEAYEVEVHRLLEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDL DVRGNHRLGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

Important features of the protein:

Transmembrane domain:

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAACCACCACAC
 CTGTTTAAAGAACCTAAGCACCATTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA
 AAGGAGGGCAGAA**ATGG**GATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGAAGTGTGTTTGG
 GTGCTGGCCTTCTCTGTGGAAGTCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA
 GATATTTCTTGAGGGAAAACACCACCAAGCAAGTGAACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCTATATTGGTG
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGGTAACTCCCATGTGCATTCT
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAATCACCACCACGCTGGGTCTGGTTGTCCA
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCT
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGGCGGA
 ATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCCTGGAAGTGGCAGCCCT
 GGTTCTGGGTTGCCTCATCCCTCTCATCTGTCTAGTAGGACACCAGCAT**TAA**ATGTTCAAGGTCCAGC
 CTGGTCCAGGGCCGTTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTTCCTCAGTC
 TCTTGTCTCACCTTGCGCATCTCTACATGTATTCTTAGAGTCCAGAGGGGAGGTGAGGTTAAACCTG
 AGTAATGGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTGT
 TATCTTTTAAAGGCCCTTGACATTTTGCCTTTAATATTTCTCTTAACCCTATTCTCAGGGAAGATG
 GAATTTAGTTTTAAGGAAAAGAGGAGAAGTTCATACTCACAATGAAATAGTATTATGAAAATACAGT
 GTTCTGTAATTAAGCTATGTCTCTTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTT
 AACATGGTTCCCAACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATA
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC
 AAGACACATTGAAAGCTCTCTTTATACTCAAAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT
 TAAACAGCTCCTTTGGCACGTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCTTGTCAAGTTCTCCTTTGCAGAAT
 ACCTGTCTCCACATTCCTAGAGAGGAGCCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCTTCAAGAA
 CAGTCAGATCACAAAGTGTCTTTGGAAATTAAGGGATATTAAATTTTAAGTGATTTTTTGGATGGTTAT
 TGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAAATGTATGGTTGTCTTTTTTTTTTGT
 TTTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCAGCTTT
 GGCGACACTGTGTCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTGCTTA
 TTGATTTAAAGCTTATTGGAATCATGTCTTGTCTCTTCGTCTTTTCTTTGCTTTTCTTCTAACTTT
 TCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTTAATATTGTTGTTGGGATGAATT
 CTTATCAGGACAACCACTTCTCGAACTGTAATAATGAAGATAATAATATCTTTATTCTTTATCCCTT
 CAAAGAAATTACCTTTGTGTCAAATGCCGCTTTGTTGAGCCCTTAAAATACCACCTCCTCATGTGTAA
 ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAAGTGTTTAACAGACTAGGATA
 ATTTTTTTTTTTCATATTTGCCAAAATTTTGTAAACCCTGTCTTGTCAAATAAGTGTATAATATTGTAT
 TATTAATTTATTTTACTTTCTATAACATTTCAAACACATTACACTAAGGGGGAACCAAGACTAGTT
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTTCTATGACGCATAAGCTAGCATGCCTATG
 ATTTATTTTCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTTGTGAGCCCTCTGCT
 GGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATTGCATACA
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT
 GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACCTATATGGTTGCCTAGATTCTCTCTGGA
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCIYAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLDQ
IGNSHVHSTDDPEAARSSNSKITTTTGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

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FIGURE 57

GCTCGAGGCCGCGGCGGCGGAGCGACCCGGGCGGCCCTCGTAGCGGGGCCCCGGATCCC
CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC
ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
CACAACCTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAA
TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA
GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
TGAGGAGCGAATAGAAGAGGTCACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAA
GTCCCAGACACCAGCCCCCAGTTCCGAAGTGGTTTTTGGATTCAAAGAGACAAGTTGAGAAAG
AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
CCAGGCCGGGAGCAGGTGGTGGAAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA
TGGAGGGCCCTGAGCGAGACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT
GCCGGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
TTTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG
AATCATACACTCTTGAATTGAACTGGAATCACATATTTCAACAACAGGGCCGAAGAGATGACTA
TAAATGTTTCATGAGGGACTGAATACTGAAAACGTGTAAATGTACTAAATAAAATGTACATCTGA

FIGURE 58

MMGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQQLQALSEPQPRQLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

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FIGURE 59

GGATGCAGAAAGCCTCAGTGTGCTCTTCTGGCCTGGGTCTGCTTCTCTTCTACGCTGGCATTGCCCTCTTCA
 CCAGTGGCTTCTGCTCACCCGTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
 TGCCATGGGGGAGCCAAGGGAAACCTGGGGCCTGCTGGATGGCTTCCCGATTTTCGCGGGTTGTGTTGGTGCTGA
 TAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTACACGTGCCTAGAGAGCCTCCTGTCTCCCTACCCT
 TCCTGGGCAAACCTAAGCTCCTTGCAGAGGATCCTGGAGATTAGCCCCACCATGCCCGGCTCTACCGATCTCAGG
 TTGACCCTCCTACCACCACCATGCAGCGCCTCAAGGCCCTCACCAGTGGCTCACTGCCTACCTTTATTGATGCTG
 GTAGTAACTTCGCCAGCCACGCCATAGTGAAGACAATCTCATTAAAGCAGCTCACCAGTGCAGGAAGGCGTGTAG
 TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGCTTTCTCCAAAGCTTTCTTCTTCCCATCCTTCA
 ATGTCAGAGACCTAGACACAGTGGACAATGGCACTCCTGGAACACCTCTACCCACCATGGACAGTGGTGAATGGG
 ACGTGCTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCCTGAAATGGCCA
 AGAAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
 CTGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTC
 TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC
 CCACGCTGGCCCTGCTGCTGGGCCTGCCATCCCATTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG
 GGGTGAGGACTCCCAGCCCCACTCCTCTGCTTTAGCCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
 CCCGATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
 TCTCCAAGGCCTCTGCTGACTACCAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA
 TTGCTGAGCTGCAGCAGTTCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGCTGCC
 GCATGGCGGGGGTACTGCTCTCTTGGCTGCTTCTGCTTTATCTGCCTGCTGGCATCTCAGTGGGCAATATCCC
 CAGGCTTTCATTCTGCCCTCTACTCCTGACACCTGTGGCCTGGGGCCTGGTTGGGGCCATAGCGTATGCTGGAC
 TCTTGGGAATATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATTCTCCCTT
 TTCTGTGGAAGCCTGGGCTGGCTGGGGGTCCAAGAGGCCCTGGCAACCCTGTTTCCCATCCCTGGGCCCCGTCC
 TGTTACTCCTGCTGTTTTCGCTTGGCTGTGTTCTTCTCTGATAGTTTTGTTGTAGCTGAGGCCAGGGCCACCCCT
 TCCTTTTGGGCTCATTTCATCCTGCTCCTGGTGTGTCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC
 TCACAATGCCCCGCTTGGCACTTCAGCCACAACAAACCCCCACGGCACAATGGTGCATATGCCCTGAGGCTTG
 GAATTGGGTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTTCATCGTTGCCCTGAAGAGACACCTGTTTGGCCT
 CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTTCGAGCCAAAGAATTTATGGTATGGAGCTTGTGTGG
 CGGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCCGCTATGGTAATCTCAAGAGCCCCGAGCCAC
 CCATGCTCTTTGTGCGCTGGGACTGCCCTAATGGCATTGGGTACTGCTGCCTACTGGGCATTGGCGTCGGGGG
 CAGATGAGGCTCCCCCGCTCTCCGGCTCCTGGTCTCTGGGGCATCCATGGTGCTGCCTCGGGCTGTAGCAGGGC
 TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCCAA
 GGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAAA
 TCTACCGACACATGCAGGAGGAGTTCCGGGGCCGTTAGAGAGGACCAATCTCAGGGTCCCCTGACTGTGGCTG
 CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTCACCCTGTTGGCCTTCCCCTTCTGCTGT
 TGCATGCGGAGCGCATCAGCCTTGTGTTCTCTGCTTCTGTTTCTGCAGAGCTTCTTCTCCTACATCTGCTTGCTG
 CTGGGATACCCGTACCAACCCCTGGTCCCTTTTACTGTGCCATGGCAGGCAGTCTCGGCTTGGGCCCTCATGGCCA
 CACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTCCAGCCATCCATTGGCATGCAGCCTTCGTGGGATTCC
 CAGAGGTCATGGCTCCTGTACTTGGCTGCCTGCTTTGCTAGTGGGAGCCAACACCTTTGCCTCCACCTCCTCT
 TTGCAGTAGGTTGCCCACTGCTCCTGCTCTGGCCTTTTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC
 CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGG
 ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCCTCAAGTACCTCTTTATCCTTGGTATTTCAGATT
 TGGCCTGTGCCTTGGCAGCCTCCATCCTTCGAGGCATCTCATGGTCTGGAAAGTGTGTTGCCCTAAGTTTCATAT
 TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGTG
 CTGTGAGCTCCTGGTTCAGGCAGCTATTTCTGGCCCAGCAGAGG**TAG**CCTAGTCTGTGATTACTGGCACTTGGCT
 ACAGAGAGTGCTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC
 TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATTCTATAATTAGGACCACAGTGGAGTA
 TGATCCCTAACTCCTGATTTGGATGCATCTGAGGGACAAGGGGGGCGGTCTCCGAAGTGGAATAAAATAGGCCGG
 GCGTGGTGACTTGCACCTATAATCCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA
 AGACCAGCCTGTGGAACATAACAAGACCCCGTCTCTACTATTTAAAAAAAGTGTATAAAATGATAATAT

FIGURE 60

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
```

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLEYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACW
MASRFSRVVLVIDALRFDFAPQHQSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRVRVFMGDDTWKDLF
PGAFSKAFFFPFNFVRDLDTVDNGILEHLYPTMDSGEWDVLIAHFLGVDHCGHKHGPHHPM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAALFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLGLPIPFNGI GEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAI SPGF PFCPLLLTPVAWGLVGAI
YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGVLLLLLLFRLA
VFFSDSFVVAEARATPFLLG SFILLLVVQLHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVL
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVLLLLFLQSFL
LLHLLAAGIPVTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHA AFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEE
L MEMRLRDAPQHFYAALLQLGLKYLFI LGIQILACALAASILRRHLMVWKVFAPKFI FEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQOR

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT
GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**ATG**T
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
TCATCACAAATTGGCCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA
TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT
ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
CCAGGACTTTGAAAGATCAATCATCAGAGTTCAGGGCTAAAATCATCTTCTGGTATGTTTTG
CCCATATCTATTACCGTGTTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAA
GATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACCTTTATCACCCCTCAATATCTCGGATGAT
TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT
CTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAAACAGTCATTGAATATGA
ATATGATGTCAGAACCACTGACATTTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGG
AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCC
CAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC
AAACTGGCAGGCTGTGTATTCCTTCGCTGTGECAGCTTCGACCAGGATTCAGAGGGCTGCGAG
CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT
TATATGTGCAGATGGAAAAC**TGA**TGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAAC
AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTTCCAGT
TTGTGAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG
GTTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGT
TGTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTTCAGG
TGGGTGT

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGKEKHPANLILYGNED
KRFFVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDKTVIEYEYDVRTTDICAGPEEQELSL
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRCLIPSLSSFDQDSEGCEPSEGDLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGTGGGCGCCACGTCCTGAGTACTGCGGAGCCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCCGAC
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC
CCAGCCCGGCCCCCTGCCTGGGACCACCAGGCCCCCAGGAGAAGCCGCC**TGAG**CCACAACCT
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTCAAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAAATGTAACTGACAAAAAAAAAAAAAAAAAAAAAGAAA

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
```

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPTQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRPLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMCTRSGDSHRRGFC SADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRRSSPQPGPLPGTTRPPGEAA

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA
CGCCTGTCCCCGGCCCGGCATGAGCCGCTACCTGCTGCCGCTGTGGCGCTGGGCACGGTAG
CAGGCGCCGCCGTGCTGCTCAAGGACTATGTCACCGGTGGGGCTTGCCCCAGCAAGGCCACC
ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC
TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTTGAAGAGGAGGAGCGAGT
GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT
TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAACTTGCTGCTGGAC
AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
GCCAGAGCAAGCTCGCCATCGTCTCTTCACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT
GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG
CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCATCTTCTGGCTGCTGGTCAAGA
GCCCCGAGCTGGCCGCCAGCCCAGCACATACTGGCCGTGGCGGAGGAACTGGCGGATGTT
TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGAGGCTGAGGATGAGGA
GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA
GGGAGCAGCCCCTCCCAGATTAACCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
ACCGAGGACAGCTGTCCGCCATGCCCCGAGCTTCCTGGCACTACCTGAGCCGGGAGACCCAG
GACTGGCGGCCGCCATGCCCCGAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGAAGTGGC
CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
AGGGGCCATCTGATGCTTCCCCTGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
TGTGCACTTGCAGGCCACGTGAGGAGAGCCAGCGGTGCCTGTCGGGGAGGGTTCCAAGGTGC
TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
TGTGCATGCATGGTCCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTG
CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
GGTGTGTTGCTGAGGGCTTCCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC
GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
TTGCCTGGGACTCCCACCTTCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC
TTGCTCATTT

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVLDILINN
AGVMRCPHWTTEDEGFEMQFGVNH LGHFLLTNLLLDK LKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGSVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTTCGCGAGCGCTGGCA**ATG**TGGTCTCTGGGGCGCGGCTGGCGGGCGCTGCTGGCGGTGCTG
GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGGCGCTGAC
CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTTCTTTGCAT
GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTTACTCTCATCAAACGCCTGCA
GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
ATGGCTATGAGAAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT
TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA
CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
ATTCCATGGCTGGAGGAGGCTGTCAGTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA
GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA
ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG
ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC
TGAGGCTGTCATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
TATGTCAGACCCTGGGTTCCAGCCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCCCTAT
GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTTCATCCACCTGGA
GCCCTACATTGCTCTCTACCATGACTTCGTGAGTCACTGAGGCTCAGAAAATTAGAGAAC
TTGCAGAACCATGGCTACAGAGGTGAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAAGTGGTGACCCTCAA
CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
TGGTGAAGTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC
AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
GGTGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
ATGCAGCACTGTTTTGGTGAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
GCTGGCTGTCCTGTCCTGGTGGGAGATAAGTGGTGGCCAACAAGTGGATACATGAGTATGG
ACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAGACT**TGA**ACTGTTGGCAGAGAGAAGC
TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTGAGCTTTGTCTGTGCCTCGCAAATCAGAGGC
AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG
AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCGATCAGTGGGTC
TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
GGGCTAGCCTGACTCCCAAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG
CAGGGAGTGTCCCCCTCCCAAGACATATCCAGATGAGTGGTACATTATATAAGGATTTTTT
TTTAAGTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTTAACACAGTCATTAAAA
ATGTTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNI PHLQTRD TYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYA EYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAAGTTTCCTGCTCCATCTCAGGAGCCCCCTGCTCCCACCCCTAG
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGGAG
CGCCCAGGATGCCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
TGGCTCAAGTTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT
GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCTTCC
TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT
GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT
CTGCCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
ACTTCCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAA
AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
GAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA
CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAACTATCGAC
AAGGAGCGTTTTAGTGTGCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
CTGGTTTCATGGACAACCTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
TCTGTCACTGATGGGCTCCTGGGGCCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
ATGCTGCTTGTGCTACCCCAATTAGGGCCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC
CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT
GCCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
GAGCCTGAGGCTCTGCTCAGGGCCCATTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA
GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTGGC
CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTA
GTTTTTTTTTACGTGATTTTTGTAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC
TAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCCAACCAGTTTGTTAA
TCAAACAATAAAAAACATGTTTTGTTTTGTTTTTAAAAAAA

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3

MPRGDSEQVRYCARFSYLWLKFSLLIIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRGIE NYDDLD FKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPG PLACGV PYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAV I IWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDG LLGPGAKPSVEAAGTGCCLCYPN

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

protein = amino acid

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
CACCTGGGAAG**ATG**GCCGGCCCGTGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC
TTGATCCAAGCCACCCTCAGTCCCAGTTCATCCTCGGCCAAAAGTCATCAAAGA
AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAAAGCCACCATC
CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTGACTGTGCCACCAGCCA
TGGGAGCCTGCGCATCCAAGTGTGTATAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGC
AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTC
CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATT
AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC
TCTGCAGCTTCCCTGACAATGCCCACCCTGGACAACATCCCGTTTCAGCCTCATCGTGAGTCA
GGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCCTGTTGG
ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA
GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC
ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG
AAGGCCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCCAG**TGA**AGACTTGGATGGCAGCCATCAG
GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
CAATAAACACTTGCCTGTGAAAAA

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881

><subunit 1 of 1, 484 aa, 1 stop

><MW: 52468, pI: 7.14, NX(S/T): 3

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGENTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLTKDALVLTASLWKPSSPVSQ

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAAC**ATG**GCGAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCCAAAGAAAGAAGGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAAGTGCATAGACAGTGTGTCGTTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
 AAACCTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTTGCCATGGTGGATTTTG
 ATGAAGGCTCTGATGTATTTTCTGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT
 CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTGCAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA
 GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGCCTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTTAGATCTAAATATCATGGCTAC
 CCATACAGCTTTCTGATGAGT**TAAA**AAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAAATCGTGTGTGTTTGAAAAGAAGAATGCAACTTGTATATTTTGTATTAC
 CTCTTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAAACCAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT
 CCCAGTGAACTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGTAAAA
 CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT
 TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC
 TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT
 ACTTTACGCATCTTTCTTTTGTAGTAGAGAAATTATGTGTGTGTCATGTGGTCTTCTGAAAATG
 GAACACCATTTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA
 GATTTTCAGATTCATTCCATCTCCTTAGTTTTCTTTTAAAGGTGACCCATCTGTGATAAAAAATA
 TAGCTTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT
 TTGTCACCTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTGAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAATCAGGAGATGGAGGTTTTCAGTGAGCCGAGATCACGCCACTGCACTCC
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVVALLIIVCDVPSASAQRKKEMVLSEKVSQLMEWTKRNPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNNGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

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FIGURE 75

[illegible]

FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSĠGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVS HDAIKIPKWSPLS
EMHPVDYYSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVVS LVDIYPTMLDIAGIPL
PQNLSGYSL LPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
 GGTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
 TGTGACATCTATAGCACCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
 ATCCTTGGAGGCCTCCTGGGATTCATTCCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA
 CTTCTACTCACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC
 CAGAGAAATCGCTCCAACTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT
 ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
 CCCTGCCCTAAGTCCCCAACCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG
 ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC
 AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNYSYSLTGYV
```

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCACTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTTG
TGAAGCTGAAGGTTTCAGGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCTTGAGAAGACATAGAAAGAAAATCAACTTTCTACTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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FIGURE 80

MVPRI FAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTND FVVKLVQGVNSQCHSSPISSKCESRRRF

Signal peptide:

amino acids 1-25

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FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGCAGTGTGAGCTAATGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACCTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT
GACCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCTTCACCCT
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM LCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDR LCRSVS

amino acids 1-24

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCCGCAGCGCTCACTCGCTCGCACTCAG
TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCGGGCACCAGAAGTTCTCT
GCGCGTCCGACGGCGAC**ATG**GGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTTCG
CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTCACCCTCACCTGCAGGCTCT
TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG
GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT
CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT
ACCCATCCTCCTCCCAGGATAGTGAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
CTCCAACCGCCGTGCCAGGAGCTGGTGCGGATGGACAGCAACATTCAAGGGATTGAAACCC
CCGGCTTTGAAGCCTCACACCTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
TCCTATGTGGCCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTGAGGCCAGCAC
CCCCCTGTCTCCTCCAGGCCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT
CTCCAAACTTTGAGGTCATC**TAG**CCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC
CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCCAGCCCCTCAACCCCTC
TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGCTGAG
ATTCTCCCTTAGAGACCTGAAATTACACAGCTACAGATGCCAAATGACTTACATCTTAAGAA
GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG
GAGAGACTTCTCCCCCGTGGCCGCCTTGGCTCCCCCGTTTTGCCCGAGGCTGCTCTTCTGTC
AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC
ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
ATGTTGCCCCACCACTGGAGATGGTGCTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA
GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCACTGCTCAGCGCGGGCC
ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
GCTATTAAAACTACATGGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLLDGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVVPSSSQ
DSENITAAALATGACIVGILCLPLILLVYKQQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

[illegible]

FIGURE 89

[illegible]

FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVRVPFPWVGTLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTQ
QWDTPCPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCCTGTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCCTCATTTCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTGTCAGTCCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG
 GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTGAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCC
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCC
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
 AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCCTCCCCAGGG
 GTGAAATG**TAG**GATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
 AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFFRPTAKWKGPQGQDLSTDSTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAEIRDARKHAVEVTLPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRLNGEHLTYFTLNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSSESSSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGLALLCCAAAAA AVASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTP LWATAGPSSTTFQAPLGPSPTTPPAAERTS
TTSQAPTRPAPTTLSTTTGPAPTPPVATTVPAPTPRTPDLPSSSNSSVLPTPPATEAPS
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLN YTSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC
CTGGGCTTCCTGTCACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT
CACAGCA

FIGURE 96

MGGLLLAAFLALVSVPRQA VWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVG VVT
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

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FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGACATGCTGCTGCTGCTGCTGCC
CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
GGCTGGATTTACCCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA
CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA
AGAAGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
GCACCCTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
GGGACACCCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
CCGCTCCTCGGTGCTCACCCCTCATCCCACAGCCCCAGGACCATGGCACCCAGCCTCACCTGTC
AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC
CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
ATTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCCGGGGGAGCTGGAGCCACAGCCCTG
GTCTTCCTGTCCTTCTGCGTCATCTTCGTTGTAGTGAGGTCCTGCAGGAAGAAATCGGCAAG
GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTTCAGCCT
CTCAGGGGCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT
TCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
ACAGATTGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCCTCCAGGCAAGGGA
GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETDRFHL LGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLT LIPQPQDHGTS LTCQVTFPGASVTTNKT VHLNVSYP PQNLMTV FQGDG
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVS LQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGD TGIEDANAVRG SASQGPLTEPWAEDSPPDQPPPASARSSVGE GELQYA
SLSFQMVKPWD SRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAG**ATGA**AAGACCCTGTTTCCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGGAGGACAGGAGGCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTCACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC**TAGG**
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAA

FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:**Signal peptide:**

amino acids 1-17

100/249

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTCGAG
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG
GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAGACCACCGCAATGA
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGGCCCTCTGGTCTGTAACCAGTCTCTT
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA
CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGTTGGTTCCTGTTCACTCTGTTAAT
AAGAAACCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCCLISGWGSTSSPQLRLPHTLRCANITIIHQKCENAYPGNITDTM
VCASVQEGGKDSCQGDGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTTCCTGCTGGAGCCG**ATG**CCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAAGTCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTTGTTCCTGGTGTGGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
TGCATACGGAAAGGAAGGCTATGCAGAAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAAGATATTTTTAAGA
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTCCCTATGAGAAGATATTTTGA
TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLGWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDFISPKEYNVYQHDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAA**ATG**CAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC
CCTTGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTG**TAA**TCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAATCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTTCCTGGGATCCCCTCCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSRL

Signal peptide:

amino acids 1-18

106/249

FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**
GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
CAGCCTGCGCTGCGGGGGTGTCCTTATTGACCACAGGTGGGTCCCTCACAGCGGCTCACTGCA
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
CAGATCCGGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC
CCCTGCCCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
GTCCTTCAAGGTCTGGTGTCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**TGAC**
CTGTTTCCTCCACCTCCACCCCCACCCCTTAACCTTGGGTACCCCTCTGGCCCTCAGAGCACC
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTGTCCTGGGAACTTCTTGGAACCTT
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

108/249

FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCGAGCTCAGCA
ACAGGTTCCAAGGAGGGAAGGCGTTCGGCTTGCTCAAAGCCCCGGCAGGAGAGGAGGCTGGCC
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTGACACTATATCCTACCGAGACTTTGTGAA
CATGATGCTGGGGAAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCC**TGA**
GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTGTGTGTTT
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGCGGGAATCC
TGAGCCTTGGGTCCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG
ATATCAAACCAAAAAGTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
CTCACTTGAGGAACAGCACTCTCCATCCTTTTCAAGAAAGTCTCCAAGCCAAGTTCAGGCTC
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
CTGCAGGGCCTCTTTCGGGTTTCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
TACCAGAAGGAACCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
GGGTTTGGGGGGAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

110/249

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV
MFEGKANESSPKPVGPPPERDIASLP

110/249

FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGCAGAGGCAGCCTCCTCCA
GGAGCGGGGCCCTGCACACC**ATG**GCCCCCGGGTGGGCAGGGGTTCGGCGCCGCGGTGCGCGCC
CGCCTGGCGCTGGCCTTGGCGCTGGCGAGCGTCCTGAGTGGGCCTCCAGCCGTCGCCTGCCC
CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGTTT
CTCGGGGCATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGATCTGGAAGACAACCAGGT
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA
GATTTGAGTGAAAACCAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCAGATGT
GAAGAACCTGCAACTGGACAACAACCATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGC
TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTACACTCT
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG
TGCCAGCCCCCCTCCTCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCCCTCGCC
CTGCACGTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCTTGCCA
ACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA
GGAGCCTTACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
TATTGCTCCAGATGCCTTCCAGGGCTGAAATCACTCACATCGCTGGTCCTGTATGGGAACA
AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCCTCTGCAGT
CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCCCGCGCCG
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
ATTACCGCAGCAGGTTTCCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG
TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC
TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
TCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
CGAGAGGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCT
GGAGACCGTGCACGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCCGGTGAGACTGCTG
TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTCACCACGCTTGTCTCCCT
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTTCCTC
AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTACCTGTGATGGCAACGAGGAGAG
TAGCTGCCAGCTGAGCCCCGCGCTGCCCGGAGCAGTGACCTGTATGGAGACAGTGGTGCGAT
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC
CTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCTTCAAC
GGGCTGCGGTCCCTGCGAGTGCTAACCCTCCATGGCAATGACATTTCCAGCGTTCTGAAGG
CTCCTTCAACGACCTCACATCTCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG
ACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT
CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC
CGTGCAAGAATAACGGGACATGCACCCAGGACCCTGTGGAGCTGTACCGCTGTGCCTGCCCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCAGCTGCTCCTGCCCTC
TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
AACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTCAGCATG
AGGCCAAGTGCATCCCCCTGGACAAAGGATTCAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCACAAGTGCCGCCACGGGGCCCAGTG
CGTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCTTCTGTG
AACACCCCCCACCCATGGTCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC
GGGGCCCAGTGCATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCGG
CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAAGTGG
CCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
GGCATCCTTCTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCAGGGCCACGT
GCGGCTGGTCTATGACAGCCTGAGTTCCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA
ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCTGAACCTAGTAGTG
GACAAAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGCACGG
ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG
GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCACCAGGCTGCAAGTCCCTGCACCGT
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
GCTGGACCGGCCCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC
CATGGAAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG
GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC
GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGGCT
GTGGGCCCCCAGTGCTGCCAGCCCACCCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG
GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC
CTAAGCCCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
ATGTGGGACCCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA
AGAGAATATTAAGTATATTGTAAAAATAACAAAAAATAGAAGTTAAAAAAAAAAAAAAAAAAAA
AAAAAA

FIGURE 112

MAPGWAGVGAAVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNLNKNKLQVL
 PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK
 GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL
 AQNPFVCDCHLKWLADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDIRSRFS
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNDTFAGLSSVRLLSLYDNRIITTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRKR
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGLR
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL
 SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCSLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFQCKGPVDINIVAKCNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEGQR
 CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLQHEAKCIPL
 DKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMV
 LLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS
 VELVTNLNQLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAATGGCAAAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGGAAGCTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGA AAAAAGGCTGTGAGGTTTCCTAAACTGGAAGCTGGACCCAGGATGCTTTGCAGCAAC
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA
TTCCTTCTCAAATTTGGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKCLKENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

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FIGURE 115

CAGGCCATTTGCATCCCCTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCTATTAAAACTTGTACATGGCTCCC
 CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTT
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCAG
 CTTTGACTCAGTTGTTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCC
 CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCCAGTCATTGCTGTTAATTCGGGTGGACCCTTGGAGT
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACTTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTTCCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTAT**TAA**TCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC
 CAGTTTTTGAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTTACGAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCAA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCAGATTCAAT
 CCACCGAAGTGTTCACTGTCTGTTAGGGAATTTTGTGTTGTCCTGTCTTTGCCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTTTTTAAAGATAATTTGTATTTTTTGCACTGAGATATAA
 TAAAAGGTGTTTATCATAAAAAATAAAAAAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFERLARRRKKILFYCHFPDLLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

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FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCA**ATG**TTGGACTTCGCGATCTT
CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT
CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC
ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
CAATCTGGTGGTGGCAGTGTGAGTGAAAACACATGAGGAAAAAATTGTATGAAAATGGTGT
GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCCTCAGCCAGCATATGCTTGGTTTTGCT
ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG
CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTCTAGATGGGTCAC
TTGATAAAAACATGACTCGGAAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTTTCATTGACTC
CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTTAACCACCTCTGAA
GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTTTTTGGAAATGGTCCTGTTACTCC
AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAAACTGTTTCGAACTGCCA
AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAAATTGACCGATTTATTATT
CCTAGAGAGACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTTCTC
CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA
GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
AT**TAA**AATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAA
AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC
TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVS LGTVDLKQHINPNKTS DPFETMLKSLLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLLLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIRFQKNHGTWVSEIGKGFLDGS LDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLT TSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDDDELVMKTFSS LGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA
GACCGCCGCCCTTGTCCTCCGAGGGCC**ATG**GGCCGGGTCTCAGGGCTTGCGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG
TGGCCGCGCTCTCTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTTGTCT
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAA
AAGAAACCCTTC**TGA**TTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
CCGCTTCGTATTCCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
ATTAAAAAAAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

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FIGURE 121

TCCCGGACCCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC
AGCAGGCCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGACGTGGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAAC TTCAGGGTGC
CCACTCAGGTCAC TTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCA ACTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TGA**GGCC
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT
 GACTCGCTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACCTACCATAGTGATACCCCCTACTACCCATC
 TGGG**TGA**ACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTCAGGCAGGGAGGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCGTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCCACACTAAGGCC
 ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACGGGGTTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGAGA
 GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGGAGGGGAGGGAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAAGCTT
 GCCCCGGGGCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY
YPSG
```

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCCA
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGGAAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTGACCTAGCCGCTAG
 CATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC
 GGCTGCGGCTGCCCACACGGCTCACC**ATG**GGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
 GCCGTGCTGCTGGTCCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
 GCTCCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG
 GCGGTGCGGAGCACCACACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
 CGATCAGATCCTGGTGAATGTGGGTAATTTTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA
 GAAAAGGAATTTACAGTTTTCAGTTTTTCACGTGATTAAAGTCTACCAGAGCCAACTATCCAG
 GTTAACTTGATGTTAAATGGAAAACAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCCACGTTTTCTGGCTTTCTGGTG
 TTCCCCCTA**TAG**GATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
 TGTGTCTGTTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTTCATTTCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTGTTGTTCTTGTA
 AAACTTGGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
 TGGCTTGCCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA
 GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
 TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCTCCGAGGGAAATCTTATACTTTATTGC
 TCAACTTTAATTAAAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTTT
 TCCGTAGACATGACCACTTTATTAACCTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA
 TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
 CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAAA

FIGURE 126

MSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGGKCLVVCDSNPATDSKGSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVVFVAPRKGIYSFSF
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

127/249

FIGURE 127

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTTGATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT**TAA**CCTCAGGGAACCAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 128

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658

><subunit 1 of 1, 257 aa, 1 stop

><MW: 28472, pI: 9.33, NX(S/T): 0

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNLTSLGPGTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKCLLCQDKN
FLLYNQSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC**ATG**TTGCTCTGGGCTTGCCCTTCT
 TGGTGCTCTTGGTGGCTCGGTGCGAGGCCATCTGGGGGTTCTGGGGCCCAAGAACGTCTCGCAGAAAGACGCCG
 AGTTTGAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCC
 GCAACAGGACAGAGGGCGTGGTGTGTCTGTGAACGTCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTTGTGG
 TCCGCCAGAAGGAGGCTGTGGTGTCTTCCAGGTGCCCTAATCCTGCGAGGGATGTTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGGAAACGAACCTGTGTGAGCCCCCACCAAGAATGAGTCGGAGATTGAGTTCTTCTACGTGGATG
 TGTCCACCCTGTCAACAGTCAACACCACATACCAGTCCGGGTGAGCCGCATGGACGATTTTGTGCTCAGGACTG
 GGGAGCAGTTGAGTTCAATACCACAGCAGCAGCCCCGACTTCAAGTATGAGTTCCCTGAAGGCGTGGACT
 CGGTAATTGTCAAGGTGACCTCCCAACAGGCCTTCCCCTGCTCAGTCATCTCCATTGAGGATGTGCTGTGCTCTG
 TCTATGACCTGGACAACAACGTAGCCTTCATCGGCATGTACCAGACGATGACCAAGAAGGCGGCCATCACCGTAC
 AGCGCAAAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCCGGGGCT
 CCTGCTCTTCTACCCCTTCGCGAGAAGATGAACCGGTGATCAAGGGCACCGCCAGAAAACCTGTGAGTGTGG
 TGTCTCAAGCAGTCAGTCTGAGGCATACGTGAGTGGGATGCTCTTTGCTGGGTATATTTCTCTCCTTTTACC
 TGTGACCGTCTCTGCTGGCTGTGGGAGAAGTGGAGGCAGAAGAAGACCTGCTGGTGGCCATTGACCGAG
 CCTGCCAGAAAAGCGGTACCCCTCGAGTCTGGCTGATTCTTTTCTGGCAGTTCCCTTATGAGGGTTACAAC
 ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTACG
 GTTACCAGGGCCGCTCCTTTGAACCTGTAGGTACTCGGCCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG
 ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTATTTCGCACCAAGCAATACCTCTATGTGGCTGACC
 TGGCACGGAAGGACAAGCGTGTCTGCGGAAAAAGTACCAGATCTACTTCTGGAACATTGCCACCATTGCTGTCT
 TCTATGCCCTTCTGTGGTGGCTGGTATCACTACCAGACGGTGGTGAATGTACAGGGAATCAGGACATCT
 GCTACTACAACCTTCTCTGCGCCCCACCTGAGCAATCTCAGCGCCTTCAACAACATCCTCAGCAACCTGGGGT
 ACATCCTGCTGGGGCTGCTTTTCTGCTCATCATCTGCAACGGGAGATCAACCACAACCGGGCCCTGCTGCGCA
 ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTACGCCATGGGCACAGCCCTGATGA
 TGGAGGGGCTGCTCAGTGTCTGCTATCATGTGTGCCCCAACTATACCAATTTCCAGTTTGACACATCGTTCATGT
 ACATGATCGCCGGACTCTGCTATGCTGAAGCTCTACCAGAAGCGGCACCCGGACATCAACGCCAGCGCCTACAGTG
 CCTACGCTGCTGGCCATTGTATCTTCTCTGTGCTGGGCGTGGTCTTTGGCAAAGGGAACACGGCGTCT
 GGATCGTCTTCTCCATCATTCACATCATCGCCACCCTGCTCCTCAGCAGCAGCTCTATTACATGGGCGGTGGA
 AACTGGACTCGGGGATCTTCCGCCGCATCCTCCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGC
 TCTACGTGGACCGCATGGTGTGCTGGTCTGCGCAACGTCACTCAACTGGTCTGCTGGCTGCCTATGGGCTTATCA
 TGGCCCCCAATGATTTCGCTTCTTACTTGTGGCCATTGGCATCTGCAACCTGCTCCTTTACTTCGCCTTCTACA
 TCATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTTTGCACCTCCGTGGTCT
 CGGGCTTCGCGCTCTTCTTCTTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAGAGTCGAGGGAGCACA
 ACCGGGACTGCATCCTCCTCGACTTCTTTGACGACCACGACATCTGGCACTTCTCTCCTCCATCGCCATGTTG
 GGCTCTTCTGGTGTGCTGACACTGGATGACGACCTGGATACTGTGCAGCGGGACAAGATCTATGTCTTCT**TAGC**
 AGGAGCTGGGCCCCTCGCTTCACTCAAGGGGCCCTGAGCTCCTTTGTGTATAGACCGGTCACTCTGTCTGTGCT
 GTGGGGATGAGTCCCAGCACCGCTGCCAGCACTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT
 GGGACAGCCATGGGGTGGCATGGAACCTTGACGTGCCCTCTGCCGAGGAGCAGGCCTGCTCCCCTGGAACCCCC
 AGATGTTGGCCAAATGCTGCTTTCTTCTCAGTGTTGGGGCCTTCCATGGGCCCTGTCTTTGGCTCTCCATTT
 GTCCCTTTGCAAGAGGAAGGATGGAAGGGACACCCTCCCCATTTTCATGCCTTGCAATTTTGGCCGCTCTCTCCCC
 ACAATGCCCCAGCCTGGGACCTAAGGCCTCTTTTCTCCATACTCCCACTCCAGGGCCTAGTCTGGGGCCTGA
 ATCTCTGTCTGTATCAGGGCCCCAGTTCTCTTTGGGCTGTCCCTGGCTGCCATCACTGCCATTCCAGTCAGCC
 AGGATGGATGGGGGTATGAGATTTTGGGGGTGGCCAGCTGGTGCCAGACTTTTGGTGCTAAGGCCTGCAAGGGG
 CCTGGGGCAGTGCGTATTCTCTTCCCTCTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCCAATT
 TGAGAACCCTCTGATTCAAGAGGCTGAATTCAGAGGTCACCTCTTCATCCCATCAGCTCCCAGACTGATGCC
 AGCACCAGGACTGGAGGGAGAAGCGCTCACCCCTTCCCTTCTTCTTCCAGGCCCTTAGTCTTGCCAAACCCC
 AGCTGGTGGCCTTTGAGTGCCATTGACACTGCCCAAGAATGTCCAGGGGCAAGGAGGGATGATACAGAGTTTCA
 CCCGTTCTGCTCCACAGCTGTGGGCACCCCACTGCTACCTTAGAAAGGGGCTTCAGGAAGGGATGTGCTGTTT
 CCTCTACGTGCCAGTCTTAGCCTCGCTCTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGTCTTCAGGCA
 AGTTCTGTGTAGTCATGCACACATACCTATGAAACCTTGGAGTTTACAAAGAATTGCCCCAGCTCTGGGCAC
 CCTGGCCACCCTGGTCTTGGATCCCCCTCGTCCCACCTGGTCCACCCAGATGCTGAGGATGGGGGAGCTCAGG
 CGGGGCTCTGCTTTGGGGATGGGAATGTGTTTTTCTCCAAACTTGTTTTTATAGCTCTGCTTGAAGGGCTGGG
 AGATGAGGTGGGTCTGGATCTTTTCTCAGAGCGTCTCCATGCTATGGTTGCATTTCCGTTTTCTATGAATGAATT
 TGCATTCAATAACAACCAGACTCAAAAAAAAAAAAAA

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFPCSVISIQDVLCPVYDLNNAVFIGMYQTMKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSPLPFYPFAEDEPVDQGHRQKTLSVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLLVAIDRACPESGHPRLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCPNYTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYYMGRWKLDSGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCILLDFFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF
```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGGCCCTGCCTTGCCCCACCCAGCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTCT
 ACC**ATG**GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCAGAAAACCTATGGTGGAATTTCCCTTTATAACC
 TGACCAAGTTGCCGCTGCCCCGTGAGGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCA
 GGCAAGGCAACTGAGGGCCCATTGTGCTATGGATCCAGATTTCTGGCTTCTGCTGGTGACCAG
 GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCACCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC
 CTTCTCTTCTTGTAGAGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
 FCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCTATACCCGCACCACATGGCCCAGGTACACTGGAGTGAGGGGTGATGT
 GCACTATCACCTGGAGAGCCATCCCCCGGGACCCCTTTGAAGTGAATGCAGAGGGAAACCTCT
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGACTAGACTGTCAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCC
 CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT
 GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGAT
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGCCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC
 AGCCGGCTCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTTCT
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC
 GCCCAGTCCCTGCAGGGCGCCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCAGGA
 TACAGCCCTGACTCTTGCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG
 GCTTGATCGTGAGTGGAACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC
 TTCACCCCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC
 CCATGCCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG
 TGGTCAGCCACAATGCCCAGATGTGGCAGCTCCTGGTTTCGAGTGATCGTGTGTGCTGCAAC
 GTGGAGGGGACAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCATGCCACGAAGCTGTGGGC
 AGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCTCATCCTCATTTTACACC
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCCTGAAGGCG
 ACTGTCT**TGA**ATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGCCCAGCACCCAAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCCAT
 CTGCCCTGGGGTGGAGGACCATCACCATCACAGGCATGTCTGCAGAGCCTGGACACCAAC
 TTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTTTGCCCAATAATAAAGCCCCA
 GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPAELSVVPEVNYGGNFPLYLTKLPLPREGAEGQIVLSGD
SGKATEGPFAMDPDSGFLLVTRALDREEQAQYQLQVTLEMQDGHVLWGPQPVLVHV
KDENDQVP HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAP
AQPSDFMQLEPRL GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEV
SIIESTWVSLEPIHLAE NLKVLYPHMAQVHWSGGDVHYHLESHPPGPFVNAEGNLYV
TRELDREAQAQYLLQVRAQN SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPEL
SPPGTEVTRLAEDADAPGSPNSH VVYQLLSPEPEDGVEGRAQVDPSTSGSVTLGVLPL
RAGQNILLVLAMDLAGAEGGFSSTCE VEVAVTDINDHAPEFITSQIGPISLPEDVEPGT
LVAMLTADLEPAFRLMDFAIERGDTE GTFGLDWEPSGHVRLRLCKNLSYEAAPSHEV
VVVVQSVAKLVGPGPGGATATVTVLVERV MPPPKLDQESYEASVPISAPAGSFL
LLTIQPSDPISTRFSLVNDSEGWLCIEKFSGEVHTA QSLQGAQPGDTYTVLVEAQD
TALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF TLGPNPTVQRDWRLQ
TLNGSHAYLTLALHWVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV EGQCMRKVGR
MKGMPTKLSAVGILVGTTLVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGAC**ATG**AGGTGGATACTGTTCAATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCACTCTGCAGGCATTTAAATCCTTCCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTTCGTTTGAAAACCGGCCGATGTATGTACTGAAGTT
 CAGCACTGGGAAAGGCGTGAGGCGGCCGGCCGTTTGGCTGAATGCAGGCATCCATTCCCAGAG
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTGCTGTGGCCAATCC
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC
 CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAG
 GGAGCCAGCGACAACCCTTGCTCCGAAGTGTACCATGGACCCACGCCAATTCGGAAGTGGA
 GGTGAAATCAGTGGTAGATTTTCATCCAAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC
 GAGGAACTCGACAAGGTGGCGAGGCTTGCGGGCCAAAGCTCTGGCTTCTGTGTGGGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC
 TTCTCCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTAC**TAG**GCGATGGCTCTGCTCTGTCTACATTTAT
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGTCTCTGGCGGTGTCCCTGCAAGAAGTGGTTCTGCCAGCCTGCTCAATTTTGGTCCTG
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTC
 AGCATCACCCCTTCCCTGGGTGGCATGTCTCTCTCTACCTCATTTTTTAGAACCAGAACATC
 TGAGATGATTCTCTACCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT
 GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTT
 TCGCAGTCTTCTGGAATAATTTTCTTTGAGCAGCAAATCTTGTAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTGTGCT
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAGCA
 ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA
 ATTTTGTGTTTTTGTAGAGACAGGGTTTCTCCATGTTGGTTCAGGCTGGTCTCAAACCTCCCA
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
 TGCCGGGCCCCGTCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTCAC
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCACTGTG
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTGCAGGATGGTGAAATTATCCCCATCTGTCTAATGGGCTTACCTCCT
 CTTTGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCCTAAATCACTCAT
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTGTGCTGTGGTGTATCCTGTGTT
 TCCTTGTCTGGTTTG
 TCTGTCTATTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCT
 GCCTCTTGTTCATTTACCTCAGCACGTACCATCTGTCTTTTGTGTTGTTGTTGTTGTTTGT
 TTGTTTTTTTTGCTTTTACCAAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDONLY

Signal peptide:

amino acids 1-16

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FIGURE 135

[illegible]

FIGURE 136

MASYLYGVLEFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

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FIGURE 137

[illegible]

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
SNGAGTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS
GASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEAST
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
GPGGNHGAPHRPRWSPNWFWRPVS SIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
CCAGCAAT**ATG**CATCTTGACAGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
CTGCTGGACAGGCCGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGAAGGAGC
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCC**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC
ATGACCTGGAGGGGTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG
GGATTTGTGAATAAACTTGATACACCA

FIGURE 140

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 141

CTCCGGGTCCCCAGGGGCTGCGCCGGGCGGCGCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
 CCCGCGGGGGCGATGACCGTGCGCTGACCGTGACTACTCCAGGTCCGGAGGCGGGGGCCCCGGGGCGACTCG
 GGGGCGGACCGCGGGGCGGAGCTGCCGCCGTGAGTCCGGCCGAGCCACCTGAGCCCCGAGCCGCGGGACACCGTC
 GCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGGCGCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGCTGCCG
 CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGCGAGCCGCCGCTCCGACCTGGGCGCTCAGC
 CCCCAGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTCTGAAGCTGAACACATCTCCAACCTAC
 ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCGTGTACGTGGGTGCTCGAGAGGCCCTCTTTGCACTCAGTAGC
 AACCTCAGCTTCTGCGAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGCGAGCGCAGAGAAGAAACAGCAGTGC
 AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC
 CTGTTACCTGTGGCACAGCAGCCTTCAAGCCCATGTGTACCTACATCAACATGGAGAACTTACCCTGGCAAGG
 GACGAGAAGGGGAATGTCTCCTGGAAGATGGCAAGGGCGGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC
 CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC
 CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC
 ATTCCTGAGAGCCTGGGCAGCTTGAAGGCGATGATGACAAGATCTACTTTTTCTTCAGCGAGACTGGCCAGGAA
 TTTGAGTTCTTTGAGAACACCATTTGTGTCCCGCATTGCCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG
 CTACAGCAGCGCTGGACCTCCTTCTCAAGGCCCAGCTGCTGTGCTCACGGCCCGACGATGGCTTCCCCTTCAAC
 GTGCTGCAGGATGTCTTCACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCTTTTCTATGGGGTCTTCACT
 TCCAGTGGCACAGGGGAACTACAGAAGGCTCTGCCGTCTGTGTCTTCAATGAAGGATGTGCAGAGAGTCTTC
 AGCGGCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG
 CCTGGAGCGTGATCACCAACAGTGCCCGGGAAAGGAAGATCAACTCATCCCTGCAGCTCCAGACCGCGTGCTG
 AACTTCTCAAGGACCACTTCTGATGGACGGGCGAGTCCGAAGCCGATGCTGCTGCTGCAGCCCCAGGCTCGC
 TACCAGCGCTGGCTGTACACCGCGTCCCTGGCCTGCACCACACCTACGATGTCTCTTCTGGGCACTGGTGAC
 GGCCGGTCCACAAGGCAGTGAGCGTGGGCCCCGGGTGCACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA
 CAGCCCGTGAGAATCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCCTCACACTCGGGCGTAGTCCAG
 GTGCCCATGGCCAACTGCAGCCTGTACCGGAGCTGTGGGGAAGTGCCTCCTCGCCCGGGACCCCTACTGTGCTTGG
 AGCGGCTCCAGCTGCAAGCACGTGAGCCTCTACAGCCTCAGCTGGCCACCAGGCCGTGGATCCAGGACATCGAG
 GGAGCCAGCGCCAAGGACCTTTGAGCGCGTCTTCCGTTGTGTCCCGCTCTTTTGTACCAACAGGGGAGAAGCCA
 TGTGAGCAAGTCCAGTTCAGCCCAACACAGTGAACACTTTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGA
 CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCTCGGCCTCCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG
 GTGGGCACCCAAACAGCTGGGGGAGTTCCAGTGTGCTGCTCACTAGAGGAGGGCTTCCAGCAGCTGGTAGCCAGCTAC
 TGCCAGAGGTGGTGGAGGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTATTATCAGCACA
 TCGCGTGTGAGTGACACAGCTGGTGGCAAGGCCAGCTGGGGTGACAGACAGTCTACTGGAAGGAGTTCCCTGGTG
 ATGTGCACGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTTATTCTTGTCTTACCGGCACCGGAACAGCATGAAA
 GTCTTCTGAAGCAGGGGGAATGTGCCAGCGTGACCCCCAAGACCTGCCCTGTGGTGTGCCCCCTGAGACCCGC
 CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG
 GGGGCCCCGAGTCTTCACTGAGTCAGAGAAGAGGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG
 TGCCCCCGGCCCCGGGTCCGCCTTGGCTCGGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGC
 TGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCCTCCGCTCTGCTCTTCTCGTGGAA
 ACGACCGTGGTGGCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
 TACCACCAGACACCCAAACAGCCGTGGCCCCAGAGGTCTTGCCAAATATGGGGGCTGCCTAGGTGGTGGAA
 CAGTGTCTCTTATGTAACTGAGCCCTTTGTTTAAAAACAATTCCAATGTGAACTAGAATGAGAGGGAAGAG
 ATAGCATGGCATGCAGCACACAGGCTGCTCCAGTTCATGGCCTCCAGGGGTGCTGGGGATGCATCCAAAGTGG
 TTGTCTGAGACAGAGTTGGAACCCCTACCAACTGGCCTCTTACCTTCCACATTATCCCGCTGCCACCGGCTGC
 CCTGTCTCACTGCAGATTACAGGACAGCTTGGGCTGCGTGCGTTCTGCCTTGCCAGTCAGCCGAGGATGTAGTTG
 TTGCTGCCGTGCTCCACCACCTCAGGGACCAGAGGGCTAGGTTGGCACTGCGGCCCTCACCAGGTCTGGGCTC
 GGACCCAACTCCTGGACCTTTCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGCGAGCTCAGGAGAGA
 TTTCGTGACAATGTACGCCTTTCCCTCAGAATTCAGGGAAGAGACTGTGCGCTGCCTTCTTCCGTTGTTGCGTGA
 GAACCCGTGTGCCCTTCCACCATATCCACCCTCGCTCCATCTTTGAACTCAAACACGAGGAACCTAAGTGCACC
 CTGGTCTCTCCCCAGTCCCCAGTTACCCCTCCATCCCTCACCTTCTTCCACTCTAAGGGATATCAACACTGCC
 AGCACAGGGGCCCCGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACCTTATGTCTATTTTTTAATAAA
 GTCTGAAGAATTACTGTTTAAAAA

FIGURE 142

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSMCTYINMENFTLARDEKGNVLLEDGKGRCF
FDPNFKSTALVVDGELYTGTVSSFQGNDAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQP
QLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVTGQQLGFEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVVIISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECAVHPKTCPVVLPETRPPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTESEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGCGGCGCCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCGA
 GCCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCGCCGCTCGTCGCCGCTCG
 TGCCGGCCCCGCTCCCCGCGCGAGCGGGAGGAGCCGCGCCACCTCGCGCCGAGCCGCGCTAGCGCGCGC
 CGGGCATGGTCCCCTCTTAAAGGCGCAGGCCGCGGCGGGGGCGGGTGTGCGGAACAAAGCGCCGGCGCGGGG
 CCTGCGGGCGGCTCGGGGGCCGCGATGGGCGCGGCGGGCCCCGCGGCGGCGGCGGCGCTGCCCGGGCCGGGCTCG
 CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCCTGCGGCGGGCGGGCGG
 GCGGCGGGCGGGCCCCGGCGGGCGGGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
 TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG
 GCCACGGCGCGCGCCAGCCCCGAGGGCTGCCGCTCCGGGCGAGCGGCGGCTTCCAGGCGGGCGGGCGCGCG
 GCGATGCGCGGGGCGCAGCTCTGGCCGCCGCTCGGACCCAGATGGCGGCCCCGCGCGACAGGAACCTTTCTCT
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAACATGGTCCAAGACAA
 TTCTTGGGAAAGTTTCACTTCTTCTCAAGTGAGGGTTCTGACACATCTGTACCAATTCCAGTAGTGCCACTACGGG
 GTGTGGACGACTCCTACCCGCCCCAGAAGAAGTCTTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA
 AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAACTTCTGAGGAGTT
 TGAACAGCAGCGAGCCCCCTCTTCTTGGGCGAGACAGGCCTGGGCACCACGGAAGAAATGGGAAAATGGCCCTGG
 AGCCTGTTGAGAATCTTGCATGGGGGGGCTGGCGTGATCATGAGCCGGGAGGTGCTTCGGAGAATGGTGCCGC
 ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAGGTGTGTCCGGAGGTTTG
 CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGCAGAACAAAAAGGGGT
 ACATTAGAGATCTCATAACAGTAAATTCACCAAGCTATCACATTACCCCCAACAAAAACCCACCTACCAGT
 ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAAATACAGCTGCACCGCGAAA
 TTGTCTGATGAGCAAATACAGCAAACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCCTTCA
 TGAGGTTTACGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAAATACTTGTATTTCGGCAG
 TTGACGGCCAGCCCCCTCGAAGAGGAATGGAATCCGCCAGAGGGAAGCCTTGGACGACATTGTTCATGCAGGTCA
 TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATATTGACTTCAAAGAGATCCAGTACGGCTACCGCC
 GGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTGCTTCTGTACAAAAGCACAAAGGGAAGAAAA
 TGACGGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTTACGAAAATCCAGTTTGTGGAGCATGAGGAGC
 TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTCTTCTCAAACCTCCCTGAAGA
 AGCTCGTCCCTTTTCACTCCCTGGGTGCAAGAGTGAGCACAAAGAACCCAAAGATAAAAAGATAAACATACTGA
 TTCTTTGTCTGGGCGTTTTGACATGTTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCCAATC
 AGAACGTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACCCTGACAAGGCCAAACAAGTTGAACTGATGA
 GAGATTACCGCATTAAGTACCCTAAAGCCGACATGCAGATTTTGCCTGTGTCTGGAGAGTTTCAAGAGCCCTGG
 CCTTGAAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCTCTTCTTCTGCGACGTGACCTCGTGTCTTACTA
 CAGAATTCCTTCAGCGATGTGAGCAAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTTCAGCCAGT
 ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCATTTTGCCTTTACTCAGAAAATGGCTTCT
 GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA
 TCCAAGGCTGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC
 AGGAAGTAGGATGATCCAGTCCACCTCCTGCTTTTGTGATCCCAATCTTGACCCCAAACAGTACAAAATGT
 GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA
 GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTAAATGTCCAGCTTTGCTGGAAAAGACGTTTT
 TAATTATCTAATTTATTTTTCAAAAATTTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC
 AAGTGGTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTGTGCTTTGAA
 CACATCTTCTGCTGAACATTATGTAGCAGACCTGCTTAACTTTGACTTGAATGTACCTGATGAACAAAATTTT
 TTTAAAAAATAGTTTTCTTTTGGACCCCTTGTCTCAGTCTATGGCAGAAAACGTGAACATTCCTGCAAAGTAT
 TATTGTAACAAAACACTGTAACCTCTGGTAAATGTTCTGTTGTGATTGTTTAAACATTCCACAGATTCTACCTTTGT
 GTTTTGTTTTTTTTTTTTACAATTGTTTTAAAGCCATTTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA
 GCTGTTTCATCATTTGCTTTCAGGAGAGCTTTCCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGC
 CACGTAGGTTTTTTGTTTGTGTTTTGTTTCTTTTTTTGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATG
 CAGTGGCGCAATCTTGGCTCACTTTAACCTCCACTTCCCTGGTTCAAGCAATTCCTTGCCTTTGCTTCCCGAGT
 AGCTGGGATTACAGGCACACACCACGCCAGNTAGTTTTTTTGTATTTTGTAGTAGAGACGGGGTTTACCAT
 GCAAGCCAGCTGGCCACGTAGGTTTTTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG
 TGGTAGTTTCATTGCGCCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTTGGCATTCTTCTCTTTCAGCCCTT
 CTCTTTAAAGGGTAAAATATTAATGTTTAGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACT
 GAAACATACACACATACACCCTAATCAAACGTTGGGGAAAAATGTATTTGGTTTTGTTCTTTTCATCCTGTCTG
 TGTATGTGGGTGGAGATGGTTTTTATTCTTTTATTACTGTTTTGTTTTATCCTTTGTATCTGAAATACCTTTAA
 TTTATTTAATATCTGTTGTTTTCAGAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTTATTTATGTGTATCGG
 GAGTGTGTTTAGTCTGTTTTATTTGTCAGTAAACCGATCTCCAAGATTTTCTTTTGGAAACGCTTTTTCCCTCC

FIGURE 143B

TAAATTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTGGAAAAATAAACAGTGAACAATATTTTTCTATTGTACTTTTGAACCATTTTGTCTCATT
ATTCCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAAGTTAAACACGAAAAA

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FIGURE 144

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMQAQKYLQTRAVAAAYRTWSKTIPGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYT
THEDVEVGRCVRRFAGVQCWVSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQEE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPMYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFSLNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESSLFFCDVDLVFETTEFLQRCRANTVLGQQIYFPPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
ACGGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC
TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTA
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
ACTTTCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
ATTCTGGTCGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATAACAAGTCACCTGTCAC
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTTGGAAGCACCCAGAGAGTTGGAATAAT
GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA
GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC
TAGATCTAAACTCTATGAATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG
CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
AAAGTTTATTAAACAATAATATAAAAAATTTTAAACCTACTTGATATTCATAACAAAGCTGA
TTTAAGCAAACTGCATTTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA
ATTTTCATATGCACTAAAAACCTAATTTAAAATAAAATTTTGGTTCAGGAAAAA

FIGURE 146

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEOPYIENEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

Signal peptide:

amino acids 1-19

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FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACA
 GGAATATCC**ATG**GGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTCTTTCCTGAGACCAGTGCAGAGGCTATGGAAGTGC GGTTCTTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC
 TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCCCAGATTTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTTCCTCCAGC
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTTTCCAGCCCTCACCTTGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCA
 GGCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGGAGTGTGTGCGGATGACGTAGACAGGGGGGAAGAACATGTG
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTAC
 ATTCAATCCCCATTTTATCAGCCTCCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
 CTGCTGACATGTCAGTTTGAAGGCTTGTTGAGACCTATATCCAGCATGCGATGTATGACGA
 GGAAAAGGGGACTCCCATATTCATATGTCCAGTGTCTGGGGAT**TGAG**ACAGAGAAGACCCTG
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC
 CCCAGCTTCCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGC
 TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT
 TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
 CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
 CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCCCTGCCTCACAGGTGAAGATTAAAGAGA
 CAACGAATGTGAATCATGCTTGCAGGTTTGAAGGCACAGTGTTTGTCTAATGATGTGTTTTTA
 TATTATACATTTTCCACCATAAACTCTGTTTGCTTATTCCACATTAATTTACTTTTCTCTA
 TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG
 GAGGTAGGATTTTTCAGTATTCTATAAGCCAGCATTACCTGATACCAAACAGGCAAAG
 AAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAACACAGACACAAAA
 TTCTAAATAAAATTTTAAACAAATTAACTAAACAATATATTTAAAGATGATATATAACTACT
 CAGTGTGGTTTGTCCCACAAAATGCAGAGTTGGTTTAAATATTTAAATATCAACCAGTGTAATT
 CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAA

FIGURE 148

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAGAGTTTGTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAA
 TTACTATAGCACATTGTTCATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA
 TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAATTTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAAATTAAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA
 GAACCCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAG
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTTGTTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGTATTTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTCTATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTTGTCAGAATTTTGAC
 TTGTTGACATAAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC
 AGCTCCTCTCATTTTCAGCAAATATCCATTTTCAAGGTGCAGAACAAAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAAATCCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT
 GGAATATTAGAAATGATCATATTCAATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAACCTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTTCATTTCCAAACAACCTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAACTTCATGCAATGTACTTGTTCTAAGCAAATTAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSVPYTNVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSONHLRQAQVTLLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG
CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG
CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCCTGCGACTACGACCACTGC
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTTCGGGCCGGCGGCCTGCCTGTGCC
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCTCCACTACTGG
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG
CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATATGTGCTTTGCGTAGTGGCCGCTA
ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
CCTGCCTTCGGGCCTTGACCCGCCTTGCGGTGCCGCCCAACCCCGCACTCTGGTCCACGC
GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
GCCTGCGGATCGCTGGGGCTGCCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCT**CTGA**
AAGGGGCCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG
GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT
GGCGCTTTGTTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTTTA
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 152

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874

><subunit 1 of 1, 238 aa, 1 stop

><MW: 25262, pI: 6.44, NX(S/T): 1

MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPFRMGVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPLNATVRRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLRDRWGCPRAAARAAGAL

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGG
 CCCAGCGCCGACGATCGCTGCCGTTTTGCCCCTGGGAGTAGGATGTGGTGAAAGGATGGGGC
 TTCTCCCTTACGGGGCTCACA**ATGG**CCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
 ATTTTGACTTACTTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTTCCTTATCAT
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGTCATGGTACT
 TTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG
 GAACTTATGGTTCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTTCAGAGAGAGTTTAAGT
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGAT
 TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTGTGGGAAGAAAATGTATTCCTTTTTTGAGAGGAACCAAACTGC
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC
 CTTGAAGAATGACAACTCTCAGCACCTGTCTGTCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTA**TAAAA**AGAAATGTCACAGAAGAAAACCAAACTTGTTTTATTGGACTTGTGAATT
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTT
 CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT
 CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACTTTC
 AATATTGGTGACTACCTAAATGTGATTTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAA
 GAGCAAGCTAACACATTGCTTAAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAA
 TCTGTATAATTCAGTCGATTTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
 ATTTGTCCGTGTATAGCATCATTATTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTA
 CCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAA
 GAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATG
 AAGACTCTTTTTGACACTAAACACTTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAA
 GCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAT
 GCTTGTGAGAATCATTAACATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTA
 ATATACTGTGGCAAATTACACAGATTATTAATTTTTTTTACAAGAGTATAGTATATTTATTT
 GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTTTATTTCTCAGAATATGGAA
 AGAAAATTAAATGTGTCAATAAATATTTTCTAGAGAGTAA

FIGURE 154

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC
 TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGG
 TGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA
 TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTC
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCCGT
 GTGGTGGGTGGGGAGGAGGCCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCCACT
 GCTTCAGGAAACATAACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAA
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCCACTCTGGATCATTGGA
 TGGGGCTTTACGAAGCAGAAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
 GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGGAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCCTTTGCAAGTGCTGGGAGCCGCTTCCTTCCTG
 CCCTGCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC
 CTCTGCCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCCTCAATTCCCTGTAAGAGACCC
 TCGCAGCCCAGAGGCGCCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
 AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACTTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTA
 CTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT
 ACCTACTGTTGTCAATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAAAAAAA

FIGURE 156

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPPIIIALLSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAEATACRQMGYSRAVEIGPDQDLVDVEITENSQELMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVC GGSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSFP SLAVAKIIIIIEFNPMYPKDN DIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCQGDSSGGLMYQSDQWHVVGIVSWG YGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGCATCCCCAGGCTCCAG
 AGCTCCCTGGTGACAGTCTGTGGCTGAGCCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCC
 TTTTCCTCTTCCAAGTCTTCAAGTCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGGCCCATGCCCA
 GGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA
 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGATATCCAGG
 ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA
 AGAAGAAGAGCAATGAGACACAGTGTTCACACTTCATCCGTGTCTGGTTTTCTTACAATGTCACCCATCTCTACA
 CCTGCGGCACCTTCGCCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTACCTGTTGCCCATCTCGG
 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG
 GGATGCTCTATTCTGGTACTATGAACAACTTCTTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGC
 CTGTCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCC
 AGGTGCTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG
 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGC
 TGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTATCCGCCACGCGGTCTCTGCTCCCCGCCGATTCTCCCA
 CAGCTCCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTTGTGCCT
 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA
 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCT
 TCATGAAGGACCATTTCTGATGGATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATA
 CACGGCTTGCAAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACCCACACAG
 GGTGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAGAGATTGAGCTGTTCCCTGACC
 CTGAACCTGTTGCAACCTGCAGCTGGCCCCCACCAGGGTGCAGTGTGTTGTAGGCTTCTCAGGAGGTGTCTGGA
 GGGTGCCCCGAGCCAAGTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCCACTGTGCCT
 GGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATT
 AAGAAGTCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTGAGCCTTGGCCTCTTATTATT
 GGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGG
 ATGGAGTTGGGGTCTCTACAGTGTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGG
 ACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA
 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTACTGGCCCCACTTGTCACTGTCACTGTCTCT
 TTGCCTTAGTGTCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG
 TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG
 AATGCAGGACCTCTGCCAGTGTGTGGACGCTGACAACAAGTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA
 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAG
 CAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGTACTCTGCATCACTGATGACACTCAGCAGGGTG
 ATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTTAACAGGGTGGGGGCTAC
 CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC
 CAGAAACACAGTGTTCAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATC
 TAAACAATCATATGCTAACATGCCACTCCTGGAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT
 TCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTC
 TTTCTGAAGTCTGACCACCTTTCTTCTTGGCTTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG
 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCTTTGT
 TTTGGGATTAGAAAACTGCTTGTGAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAAA

FIGURE 158

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDAFVAAIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGS LHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG
 TGAGCATGGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCTGCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGG
 TGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAACTTCGACATGGTGATA
 GTTGAACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC
 CATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTT
 CAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GGTTCAATTAACCTGACTTTGCCTTTGATTTTGTCTCGACCTCTGCTTCCCAACACTGTTTAT
 GTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTGC
 CAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGA
 ATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCAGTGTTCTCATTGGCCCCAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGA
 CTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCG
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
 GGAGACCAGCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTTCAGTT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGCGGCAGTGGCTGCCAGTGTCTCATCTGCGCTCCCACCCGCTCAGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGC
 TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
 GCGATGTCACCATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC
 TAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT
 CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG
 GACCACTGACCCTCAGATTTCCAGCCTTAAAAATCCACCTTCCTTCTCATGCGCCTCTCCGAA
 TCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTTT
 TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAGGGC
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCT
 TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACA
 CGGTTATCTCTCCCAACCTCACTAA

FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF
INSDFAFDFAFARPLLPTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVIWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIOHGVPMVGIPLEFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVLLGLT
LGTLLWLCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCCGTCACACACACATACCATGTT
 CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAACTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTCAGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGGCAGA
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCCCTCAGCC**ATG**TTGGGAGCCAAGCCACACTGGC
 TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGTTCTGGTGCTTCTGGCCCTGGGGGCC
 GGGTGGGCCCAGGAGGGGTTCAGAGCCCGTCTGCTGGAGGGGGAGTGCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGGCCCGGGGGAGCAGCCCTGGGAGAGGCACCCCCCTGGGC
 GAGTGGCATTTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCATGTGGTGAAGG
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCATCTCAGCC
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGA
 CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCCGGGGGAATCTACTGGGTGGTTGGAAATACT
 CAAGTTTCTCTGGCTTCCCTCATCTTCCCTCTCT**TGA**GGACCCAAGTCTTTCAAGCACAGAAT
 CCAGCCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAAGTTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCCACCCACCCACCCCAAGTTACC
 CTCCCAGCCACCTGCTGCATCTGTTCCCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA
 AGAAGGAAGATCTGCACTACTTTGCGGCCTCTGCTCCTCCGGTTCACCCACCCACCTTCCCT
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCAG
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCCTGTGAGGAAAGCCAGCATCACGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC
 CTTTGAAGTTTGAACTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCTCTCCAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTTCTCCTGAT
 CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCTTATTACCTGGGATTCCATGATTTCATTCCTT
 CAGACCCTCTCCTGCCAGTATGCTAAACCCTCCCTCTCTCTTTCTTATCCCGCTGTCCCAT
 GGCCAGCCTGGATGAATCTATCAATAAAACAAGTAGAGAATGGTGGTCAGTGAGACACTAT
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAATAAATATCAAAGTGTATACTAAAATTAAAA

[illegible][illegible][illegible][illegible]

[illegible]

FIGURE 164

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184

><subunit 1 of 1, 388 aa, 1 stop

><MW: 43831, pI: 9.64, NX(S/T): 3

MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVDWNTPKKGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEESWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-
245, 318-323, 378-383

FIGURE 165

GGGCGGCGGGATGGGGGCCGGGGCGGGCGGGCGCCGCACTCGCTGAGGCCCCGACGCAGGGCCGGGCGGGCCCA
 GGGCCGAGGAGCGCGGCCGAGAGCGGGGCCGAGGCGACGCCGGGGACGCCCCGCGCGACGAGCAGGTGGCG
 GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGGA
 CGGCTGTCTCAGCGAGGGGCCGTGCACCCGCTCCTGAGCAGCGCC**ATG**GGCCTGCTGGCCTTCTGAAGACCCA
 GTTCGTGCTGCACCTGCTGGTCGGCTTTGTCTTCGTGGTGAGTGGTCTGGTCATCAACTTCGTCCAGCTGTGCAC
 GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA
 ACTGGTCATGCTGCTGGAGTGGTGGTCTGCACGGAGTGACACTGTTACGGACCAGGCCACGGTAGAGCGCTT
 TGGGAAGGAGCACGCAGTCATCATCCTCAACCACAACTTCGAGATCGACTTCCTCTGTGGGTGGACCATGTGTGA
 GCGCTTCGGAGTGCTGGGGAGCTCCAAGGTCCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGGCTGGAC
 GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG
 GCGCTGTGCGACTACCCCGAGTACATGTGGTTTCTCCTGTACTGCGAGGGGACGCGCTTCACGGAGACCAAGCA
 CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG
 CTTCAACCACCGCAGTCAAGTGCCTCCGGGGGACAGTCGCAGCTGTCTATGATGTAACCCTGAACCTCAGAGGAAA
 CAAGAACCCGTCCTGCTGGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCTCT
 GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGAGAAGGACGCGCTCCA
 GGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAGCCTGCCCGGAGGCCGTGGACCCTCCTGAA
 CTTCTCTGCTGGGCCACCATTTCTCTGTCTCCCTCTTCAGTTTTGTCTTGGGCGTCTTTGCCAGCGGATCACC
 TCTCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCCTTTGGAGTTCGCAGACTGATAGGAGAATCGCT
 TGAACCTGGGAGGTGGAGATTGCAG**TG**AGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
 CAGTCTCAAAAAAAAAAAAAAAAAACAAAAAACCAGAAATTCCTGGAGTTGAACTGTGTAGTTACTGACATGAAAA
 ATTCAGTAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
 TTTCAAGCTAATGAAAAAGAATGAAGGAAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA
 CATATGCATGATGAGAGTCCCAGAAGGAGAGGAGAGAAAGGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA
 GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTAT
 AATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGATCTTG
 ATCAGATTAACAGCTCATTTCTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
 AACCTTCAACTGTAATTATTGGACTTTTGAGTCTTAGATGGTCCTGACCTCTTTGTCTTCAGGGACAGTTTTTCA
 ATTTAATCCCTAATAACAATTAGTCAAGCTTCCTTGACCTGTAGGAAGGCCTGTCTTTAGGCCGGGCACAGTGGC
 TTACACCTGTAATCCAGCACTTTGGGAGGCCAGACGGGTGGATCATTTGGGGTCAGGCTGATCTCAAACCTCT
 GAGTTCAGGTGATCTGCCCGCCTCAGCCTCCCAAAGTGTTGTGATTGCAGGCGTGAGCCACTGCCCTGGCCGGA
 ATTTCTTTTTAAGGCTGAATGATGGGGCCAGGCACGATGGCTCACGCCTGTGATCCCAAGTAGCTTGATTGTA
 AACATGCACCACCATGCCTGGCTAATTTTTGTATTTTAGTAGAGACGTGTTAGCCAGGCTGGTCTCGATCTCCT
 GACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTTGA
 GCATCTTGTGATGTGCTTATTGGCCATTTGTATATCTTCTATCTTCTTTGGGGAAATGTCTGTTCAAGTCCTTTG
 CCTTTTTAAATTTTTATTATTTATTTATTTATTTATTTTGTAGACAGGGTCTTGTTCTGTTGCCAGGCTGGAGTA
 CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGT
 AGCTGTATTTTTTTGTATTTTGTATTTGTAGCTGTAGTTTTTTGTATTTTTTTGTGGAGACAGCATTTACCATGA
 TGCCCAGGCTGGTCTTGAACCTCTGAGCTCAAGTGATCTGCCTGCTTCAGCCTCCCAAAGTGCTGGGATTACAGA
 CATGAGCCACTGCACCTGGCAAACCTCCAAAATTC AACACACACACACAAAAAACCACTGATTCAAATGGGCA
 GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG
 CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCTGTCTC

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVVSGLVINQVQLCTLALWPVSKQLYRRLNCRSLAYSLWSQLV
MLLEWWSCTECTLFQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFSFVLGVFASGSPLLILTLFLGFVGAASFGVRRRLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCCTGGGATCTGCCTATACCTTCTT
TTCTCTAACCTGGCATAACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCTGCCCCCTGGCCAGCTTCATTGT
ACATGTGGTGTTCTCTTGTCTTCCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCT
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC
ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
CTTGTTTAAATGCTCTCATAAGACCATTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA
TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCCCAGAATGCCCAGCTCTGAGC
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
GATGGTGTAGGGCCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA
TGCAGGTCCTGATTCAGTAGGCCCAGGTTGGGCATCTCTAACAAACTCCCACGTGATGCTGA
TGCTGGTCCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
TCAAGACTAGCCTGGCCAACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTG
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHS LQCPGAATRH IHL CVCF SFAL ALGH FLL ISLV GKGL SLSC GVGGR QAGL RLIR PWVRR
EGKINFY TNGDSW GLRP ASSVK FLGS AYTF FSLT WHTLL KASQG FSL FLGSK YLEL QEPSWS
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:**Signal peptide:**

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
 ATTAAAATCTGTTTTTTGTTCTCTTGTAAGTACGCTTTACCTTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC
 ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGA
 GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTT
 CATAGGCGATGGCTCCCAGTCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCAT
 CTAACCTTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
 AAGCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCAATTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
 GGGAAGGAACTTGTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGC
 ATCGAGTCTCCTGCATTTCAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
 CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCTCCTTCCCTC
 TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
 GCTCAGTGTTGGCCCAGGAGGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
 AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT
 CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAA
 TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
 CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTG
 GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAAAGAATTATGGTTATTTGTAA

FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVMFCSLVTSLYLPNTEDLSLWLPKPDHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

Signal peptide:

amino acids 1-15

172/249

FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
CCGCCGCCTCCTGCCCGCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT
GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGG
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
CCTGGAGCAGCCGAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
GCCCCCGGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC
GGCTGAAGCCCGCCTTGAGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCCTGTGGCGCGGGAAGGTGCTGC
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
GACGTCAGGGTCTACATCAGCCTCCTGCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
CCTGAGTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAAA

FIGURE 172

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAFAFATGLFLGRRCPWPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSRLRLLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPPELGRPLWRQAEAEHKIDLRLLKPALETLDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

[illegible]

FIGURE 174

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIIDDIADGAVKPPPNKYPIFFFFGTHETAFLGPKDLFPYD
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDERD
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSSSDSDSVKPKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEEREAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAQKPVKVERTKRSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMEKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEKLAGEEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLD RPGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATTA
 ACACCATTTGAAAGAGAACATTGTTTTTCATC**ATGA**ATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA
 TTTTCACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTTCTTCCAGTCACTGGCACTTTGAAGCA
 AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCCTTTTTGGGTTCATC
 AGAAGGACTGGATTTTCAAACCTCTTCTCTTAGATGAGGAAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT
 CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTTAAAGAAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGA
 ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTTCATCAGAGTACTTCAGCCCTATAACAA
 AACTCACATATATGTGTGTGGAAGTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
 GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCTTTTCGATCCTCAGCAGCC
 TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATACTGCATT
 CACTCGATCCCTTGGGCCTACTCATGACCACCACTACATCAGAACTGACATTTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTTATTGGAACCTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTTCG
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGAATGATGT
 AGGAGGACAACGCAGCCTGTATAACAAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
 TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
 AGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT
 CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAT
 TCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCAGA
 TGATGTCATCAGTTTCATAAAGCGGCACCTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT
 CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCATTGCAGAAGATGGCCAGTACGA
 TGTAATGTTTCTTGGAAACAGACATTGGAACCTGTCCTCAAAGTTGTGAGCATTTCAAAGGAAAAGTGAATATGGA
 AGAGGTAGTGTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTGTCTCTGAAGCA
 GCAACAATTGTACATTGGTTCCCAGAGATGGATTAGTTAGCTCTCCTTGCACAGATGCGACACTTATGGGAAAGC
 TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCCTGGGATGGAATGCATGCTCTCGATATGCTCCTAC
 TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCAATCACCCAGTGTGGGACATCGAAGACAG
 CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC
 TAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTCAAGGGATGAGCATCGAGAGGAGTTGAAGCCCGA
 TGAAGAATCATCAAAACGGAATATGGGCTACTGATTGCAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG
 CAAAGCCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCATTGAGAATGAACAGATGGA
 AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
 CTACATCCAAATCCTTAGCAGCCCAAACCTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG
 GAGACAGAGAAACAAGGGGGGCCAAAGTGGAAAGCACATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACG**TAG**TTTTCTACTTAATTTAAAGAAAAGAATTCCTTACC
 TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTTGCTAAGG
 CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAATTCATTTGAACCAGTTTT
 CCAAGAACAATCTTGACAAGCAAAAGTATAAGAATTATCCTAAAAATAGGGGGTTTTACAGTTGTAAATGTTTTA
 TGTTTTGAGTTTTTGAATTTATTGTGATGTAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGATAAGGT
 GCTTTATTCCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT
 CATTCCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTGAGACACAAATTAAGACAACCTCCCATTATC
 AACAGGAACCTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC
 TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT
 ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA
 GCTCTACAGGGACAGATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTTAATAAAACAAGGAAAACA
 TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT
 AAATCTGGCTTTGGGGAAGAACTCATATCCCCATGAAAGGAAGAACAATCACAAATAAAGTGAGAGTAATGTAA
 TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAATCTAGATTATAACA
 AACTGCTAGCAAAATCTGAGGAAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTATATAACC
 AATGATATTTTCAGTATATATTTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTATTTCTTTTTACTGC
 CTTTATTCTCTCCTGTATATTGGATTTTGTGATTATATTTGAGTGAATAGGAGAAAACAATATATAACACACAGA
 GAATTAAGAAAATGACATTTCTGGGGAGTGGGAGATATATATTTGTTGAATAACAGAACGAGTGTAATTTTAAAC
 AACGGAAGGGTTAAATTAACCTTTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAATT
 GTAGTATTGTTTTTGAATTTAACAATAAATAAGCCTGCTACATGT

FIGURE 176

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
GSSEGLDFQTLILLDEERGRLLLGAkdHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRSSQEGSTSDKTILSRVGRVCKNDVGGQQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSSISKEKWNMEEVVLEE
LQIFKHSSIIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHETADEKVI FGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKKRNRRHHRDLDELPRAVAT

```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTATCCTGGAGCATGCCACCCGCGGGGAGCAGA
 CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCCAC
 CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTCTCTGGAGTGGGAGCAGAAGGCGTGGCTGGCAAGA
 GTGGCCTGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCCGTGAATACAAGATCCAGAACCATGGGCATC
 GGGTGAGGTGGGGGGGCACAGGTGTCATGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
 AGCCATTGAGGGTGTCTGAGCTACAGAGGGGAGGGAAAGGTATTTAAGGTAACAGTGTGGCACAATAGTTAA
 GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTCTCTTCTGTTGCTTCCTAGTTCTGTAGCCCCAGGT
 AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT
 AGGGAAGATTAAATGACATAATGTATGTGATGCACTAGCAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
 TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCGAGAGAGCATCCGCCGGGCACAGGTGAGCC
 AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGGGGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTCTCTC
 CAACCGCTGAGGATGCTGAGCTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC
 CCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTCTGCTATCAGGCAGGGCGTGAGGATG
 AGCTGACAATCACGAGGGTGAGTGGCTGGAGGTATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
 ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCCAGAGAGCAGCC
 AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGCATTCTGGCACAGGGCCCTGTACAGCTACACCGGACAGA
 GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCGGGGCCAAGATGGAGTAGATGACG
 GCTTCTGGAGGGGAGAATTTGGGGGCCGTGTTGGGGTCTTCCCTCCCTGCTGGTGGGAAGAGCTGCTTGGCCCC
 CAGGGCCACCTGAACTCTCTGACCTGAACAGATGCTGCCGTCCCCTTCTCCTCCCAGCTTCTCCCCACCTGCAC
 CTACCTCTGTGTTGGATGGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTTCTGG
 ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCGGCTAAAGCCCCGGATCCTGGCCACC
 CAGATCCCCCTCACCTGCAAGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGCTGCTTCTTCAAGCTGTCTAGA
 CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCCTCACCTCCAAGGGT
 GGAAACTTGCCCCCTTCCATTTCTAGAGCTGGAACCCACTCTTTTTTTTCCATTGTTCTATCATCTCTAGGACC
 GGAATACTACCTTCTCTTCTGTCTGACCTATCTAGGGTGGTGAATGCCTGAAATCTCTGGGGCTGGAAACC
 ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTTCCCCACCCTGGCTCCATGACCCACCCCACTCTGGATG
 CCAGGGTCACTGGGGTGGGGCTGGGGAGAGGAACAGGCCTTGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
 CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCCTGGGCCTCTGTG
 CTAAGAGGGCAGGGGGCCTACGGTGTCTATTGCTTTAGGGGGCCACCACGGGCAGGGGCCTGCTCCCAGCTGCCAC
 GCTCTATCATATGGACGAGGCTGTTGGGGAAGGCGGGGCAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAC
 TGAGGGGCTGTGACCTCTCCTGAGGCCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
 AGCTGGGGGGCAGTGCTGTCCAGTGGAGGGGAGGGCTTTACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG
 TCCATCAGCACAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTTGCTTCCTGTTCAAGCTGTGTCCAGC
 TTTTCCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC
 AGTTTACTCTGGGGTTTCAGGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA
 TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG
 TCAACAATGAGAGACCAGGAGTAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCCAGCCCAGTGC
 AGTCCCGCTGTGTTTTCTACCTGGTGATCAGAAGTGTCTGGTTTGCTTGGCTGCCATTTGCCTCTTGAGTGG
 GCAGCCCTGGGCTTGGGGCCCTCCCTCCGGCCCTCAGTGTTGGCTCTGCAGAAGCTCTGGGGTTCCCTTCAAGTG
 CACGAGGGGTTAGGCTGCTGTCCCTGAGTCTCCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
 TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCAGACCCCTGACCACCCCTG
 GGTCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT
 TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG
 GCCCTCCCCCTCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCTTCTC
 AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAAGCCCACTT
 TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCACCTGCCCCACCTGCCCCA
 CAGAGAACACAGTGGTCTCCCTGTCCGGGGCGGCTTTTCCCTCCTTGGAGCGTCCCTGACGGACAAGTGAGG
 GCCTCTTGTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC
 CGTCTGAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCCT
 TCATGTTTTGTTTCTTACGTTCTTTCAGCATGCTCCTTAAACCCAGAGCCCAATTTCCCCAAGCCCCATTT
 TTTCTGTCTTTATCTAATAAACTCAATATTAAG

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEPPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSPLESSQSDSNPCGAEPFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

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FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCAGACAGAGTCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG
GCACCTCTCCCAAGCCCAAGGACTAAGTTTCTCCATTTCTTTAAACGGTCTCAGCCCTTCTGAAAACCTTTGCC
TCTGACCTTGGCAGGAGTCCAAGCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGGAGGACTTGGT
GCCCTAGACGGCTCAGTCCCTCCCAGCTGCAGTACCAGTGCC**ATGT**CCCAGACAGGCTCGCATCCCCGGGAGGGG
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCCAACCTGCCTCCTGCTCCCCATTGTGCCGCTCTCCTGGCTGGTGTG
GCTGCTTCTGCTACTGCTGGCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCCCTCCCCGGGAGGAGAGAT
CGTGTTCAGAGAAGCTCAACGGCAGCGTCTGCCTGGCTCGGGCGCCCCCTGCCAGGCTGTTGTGCCGCTTGCA
GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGCTGACAGTGCAGTA
CCTGGGCCAGGCGCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGGAGCCCTGTTAGGCGTGTTACAATATCGGGGGGCTGAACCTCA
CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCCTACGCCGGAAGAGTCC
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGGAAAGCCCCAGCCCCAGAGAGCCAA
GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCATTCCACGGTGC
GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCTTCAAGCACCCAAGCATCCGCAATCC
TGTCAGCTTGGTGGTGAAGTCCGGCTAGTGATCCTGGGGTCAAGGAGGAGGGGGCCCCAAGTGGGGCCCAGTGTCTGC
CCAGACCTTGGCAGCTTCTGTGCCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA
CACAGCCATTCTGTTTACCCGTGAGGACCTGTGTGGAGTCTCCACTTGCACACGCTGGGTATGGCTGATGTGGG
CACCGTCTGTGACCCCGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCA
TGAAGTGGGTGATGTCTTCAACATGCTCCATGACAACTCCAAGCCATGCATCAGTTTGAATGGGCTTTGAGCAC
CTCTCGCATGTGATGGCCCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGCCCGCTT
CATCACTGACTTCTTGGACAATGGCTATGGGCACTGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCTGT
GACTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGGCCGACTCACGCCATTGTCC
ACAGCTGCCGCCGCCCTGTGCTGCCCTCTGGTGTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAAAACA
CTCGCCCTGGGCGGATGGCACACCCCTGCGGGCCCGCACAGGCCCTGCATGGGTGGTGCCTGCCCTCCACATGGACCA
GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGTCTTGGGGACCATGGGGTGAAGTGTCTCGGACCTG
TGGGGGTGGTGTCCAGTTCTCCTCCCGAGACTGCACGAGGCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG
CCGCCGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
GTGTGCTGCCTACAACCACCGCAGGACCTCTTCAAGAGCTTCCAGGGCCCATGGACTGGGTCTCTCGCTACAC
AGGCGTGGCCCCCAGGACCAAGTGCACCACTCACCTGCCAGGCCCGGGCACTGGGCTACTACTATGTGCTGGAGCC
ACGGGTGGTAGATGGGACCCCTGTTCCCCGGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCCATGCTGG
CTGTGATCGCATATTGGCTCCAAGAAGAAGTTTGACAAGTGCATGGTGTGCGGAGGGGACGGTTCTGGTGTGAG
CAAGCAGTCAGGCTCCTTCAGGAAATTCAAGTACGGATACAACAATGTGGTCACTATCCCCGCGGGGGCCACCCA
CATTCTTGTCCGGCAGCAGGGAACCCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
TGCCCTCAATGGTGAATACAGCTGATGCCCTCCCCACAGATGTGGTACTGCCTGGGGCAGTCAGCTTGGGCTA
CAGCGGGGCCCATGAGCCTCAGAGACACTGTAGGCCACTGGCCAGCCTTTGACACTGCAAGTCTCT
AGTGGCTGGCAACCCCAAGACACAGCCTCCGATACAGCTTCTTCTGCCCCGGCCGACCCCTTCAACGCCACG
CCCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCGGCGGCGCCCCCTGGGCGGGCAG
GAAAT**TAA**CCCTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT
CTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCTCCTCTCTGCCCTAAT
GCGCAGGCTGGCCCTGCCCTGGTTTCTGCCCTGGGAGGCAAGTGGGTAGTGGATGGAAGGGGCTGACAGAC
AGCCCTCCATCTAAACTGCCCCCTGCTCCCCGGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCCATGCTGG
CAGTTGTATTTATTTAGTATTTATTTCACTTTTATTTAGCACAGGGAAGGGGACAAGGACTAGGGTCTTGGGAA
CCTGACCCCTGACCCCTCATAGCCCTCACCCCTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATAAGTGGTG
TGTGTATGCGTGTGTGTGTGTGTGTGAAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTTCTC
TTCCTGAATTTTATTTTGGGAAAAGAAAGTCAAGGGTAGGGTGGGCCCTCAGGGAGTGAGGGATTATCTTTT
TTTTTTTTTCTTTCTTTCTTTCTTTTTTTTTTTTGGAGACAGAATCTCGCTCTGTGCCCCAGGCTGGAGTGCAATG
GCACAATCTCGGCTCAGTGCATCCTCCGCTCCCGGTTCAAGTGATTCTCATGCCCTCAGCCTCCTGAGTAGCTG
GGATTACAGGCTCCTGCCACCACGCCAGCTAATTTTTGTGTTTTGTTTTGGAGACAGAGTCTCGCTATTGTG
ACCAGGGCTGGAATGATTTCAAGTCACTGCAACCTTCGCCACCTGGGTCCAGCAATTCTCCTGCCTCAGCCTCC
CGAGTAGCTGAGATTATAGGCACCTACCACCACGCCCGGCTAATTTTTGTATTTTAGTAGAGACGGGGTTTCAC
CATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTTAGGTGATCCACTCGCCTTCATCTCCCAAAGTGCTGGGATT
ACAGGCGTGAGCCACCGTGCCTGGCCACGCCCACTAATTTTTGTATTTTAGTAGAGACAGGGTTTACCATTGT
TGGCCAGGCTGCTCTTGAACCTCCTGACCTCAGGTAATCGACCTGCCTCGGCCCTCCCAAAGTGCTGGGATTACAGG
TGTGAGCCACCACGCCCGGTACATATTTTTTAAATTGAATTCTACTATTTATGTATCCTTTTGGAGTCAGACAG

FIGURE 179B

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTTCTCATTTGCCAATAATAATACCTCCCTTAGAAG
TTTGTGTGTGAGGATTAAATAATGTAAATAAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAGGAAA

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FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLLASLLPSARLASPLPREEEIV
 FPEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
 GTYLTGTINGDPESVASLHWDGGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHLRRKSP
 ASGQGPCMNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
 AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF
 DTAILFTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
 NSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
 PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
 PAQACMGGRCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRVPVPRNGGKY
 CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCK
 LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
 SGCSKQSGSFRKFRYGYNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
 MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
 PSTPRPTQDWLHRRRAQILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
 172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
 582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCT
AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG
ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA
TTAAAGTGATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
CCTGCCAACGAAAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATGCCTTGTAAGTGGTGGGTGGCCC
GCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATAT
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
AAAAAAAAAAAAAAAAAAAA

FIGURE 182

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727

><subunit 1 of 1, 317 aa, 1 stop

><MW: 37130, pI: 5.18, NX(S/T): 3

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTIVLFWGSKHFWPEVPPKAY
 DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKT
 QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWWPAEKPIENRDFLKNSKILEICDNVTMYWI
 NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
 TENGIEFDPMLDERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV
 ARMLGRV

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC
CGGCTGGCCTAGGCAGGCAGCCGCACC**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG
TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
GCGCCTGCGCCGTTCATCGGGATGAAGTGACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT
CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA
AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
GGCACCTTGCTTTGCCTGTCCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCC
CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
AATGGAGGCAGGGGTTCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA
ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT
TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ
DEAPYRYPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC
 CATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGGATCATGTTTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
 GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTTTACAGACCAGGTACACATTTGGTGCGGCTCTGTTTCGTG
 GGCTGGGTGCGTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
 CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTG
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA
 AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
 TTCTTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC
 ATTTTGATGATTTAGACAGACTCCCCCTCTTCCCTCCTAGTCAATAAACCCATTGATGATCTA
 TTTCCCAGCTTATCCCCAAGAAAACCTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT
 CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG
 TGATCTTAAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTG
 CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAG
 TCCTCTTTCTGTGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT
 TTAAGTCCTAAATATAGTTAAAATAAATAATGTTTTAGTAAAATGATACTATCTCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA
 ACTAATTCTTTAA

FIGURE 186

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV
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Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAAACTCATCCCAGAGGATA**ATG**GCAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
 AGAGTGTCGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAGAACTTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
 CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
 TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTGTATGTTTTTTTAACTTTACTATAAAGC
 CATGCAAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAAGAACTTTGATTTA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA
 GCTATTTTCAGCAGAATGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTTATCATTTACTTCAAATGACATTGCT
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGA
 AGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTG
 TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTT
 TTCTTGTTGATTAAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAAATATTTTTGTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACA
 ACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG
 TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTGTACCATTCTGTTTAGTTTTACTAAA
 ATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAACTGACAATCCAATTTGA
 AAGTTTGTGTGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA
 TTAATAAATTGTACATTTTTTCTAATT

FIGURE 188

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCC**ATG**GCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTGCGCTTGCTGGTCTACCTTGCTGGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA
TTGTCTTTGTCATCTCAGGGGTCTTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGGTTGCTGTGCTGCACTT
GCCCCTCGGGGGGGTCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCCCT
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCT**TGA**CGTGGAGGGGAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGT
CGTACCTTTTGTCTCTGCCTCCTGCTATTTTTCTTTTGAAGGATATTTAAAATTCATTT
GAAAACCTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
CAGTCAAGCTATGGAACCTAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
TGTCCCCAAGAGTTCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTCACCCCTGGAAAAACAAATCATCTG
TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCCCTCCGTCCTGATAAGACG
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCCTGCCCCCTCGTCTCACCCCTTTACACTCACATTTTATCAAATAAAGCATG
TTTTGTAGTGCA

FIGURE 190

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGPPSHYMARYSTSAPAISRGPPSEYPTKNYV

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

193/249

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAAGGCTTCCACGTTCTACATCTTG
AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATT TTTATCCC
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCCTTGGCATGGTGGGGACTCTTGCCACAACCCT
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGTCAGCAACATTATTGTCTTTGAGAGGCTC
TGGGAAGGGCTCTGG**ATGA**ATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
TAGCTCCTTGTTGGCTCTCCCGCCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
GGCTCTAACGAGAGGGGCCAAAGCATACCTTCTGGGAACTTCAGGAGTCCTCTTCATCCTGAC
GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
AGCGCTGCTGTCCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCT**TAA**TGCCTCCTTTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAACTGTAAGTATGTGAGGCAGGA
GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA
GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

FIGURE 192

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLS KTSTSYV
```

Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCATCA
CATACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACCTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAAACACGTCAATAAAAAAATAATCTCCCAGA

FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN

ECHLCTESLKSNGRVQFLHDGSC

Signal peptide:

amino acids 1-19

protein sequence

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCCATGGCTGCCTCCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTC
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

FIGURE 196

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
```

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLCWGPGGISGNKLLMLQKREAPVPTKTKVAVDENKAKEFL

GS LKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDYYQRHYD

EDSAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCCGCCGGAAGTGCCCGAGGGCGCGATGGAGCTGGGGGAGCCGGGCGCTC
GGTAGCGCGGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
CGTCCTTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCCTGGGTCTCAACGCACA
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCCAGCCCAGC
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTTACAGCAACACCGCCAG
CCCCGGACTCCCCGCAGGAGCCCCTCGTGCTACGGCTGAAATTCTCAATGATTGAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG
GCAGCCTTACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
CCAAATCCCCCCTGCCCGCCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT
GCTGCTGCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTACCCCTGCTCCTCAGTCTCCTG
GCCTTTGCCATGTACCGCCCG**TAG**TGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC
GGACCTTGCTCCCCGCGCCGCGGGCAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG
CCTCTTCCCGCTGCCCTGGAGCCAGCCCTGCGCCGCAGAGGACTCCCGGGACTGGCGGAGG
CCCCGCCCTGCGACCGCCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
CTGGGAGTGGGCTCCTCGGGGTCGGGCATCTGCTGTCGCTGCCTCGGCCCCGGGCAGAGCCG
GGCCGCCCCGGGGGCCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCTCCAATCCCTGAC
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTTCGGTGGGAGGCTGGTGAAGGGGAGCGGGGAG
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAAA
AAAAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRLLKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLLLWYCQIQYRPFFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

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FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCCTCCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGC
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG
AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAGGCATCCACTGCGCAAAAAGGA
TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTTCAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATTGAAACAGGGTGCGGGTGACCGTGG
AGTCATTCCAAGACTCCTGTCCTCACTCAGGGATTCTTCATTTCTTCTTCCTACTGCCTCCA
CTTCATGTTATTTTCTTCCCTTCCCATTACAACTAAACTGACCAGAGCCCCAGGAATAAA
TGGTTTTCTTGGCTTCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTAT
TTGTAAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLC HVDCQDLLNP NLLAGIHCAKRIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

CTGACCTGACTGGAAGCGTCCAAAGAGGGGACGGCTGTACGCCCTGCTTGACTGAGAACCCTG
CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAG
CAGAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTC
AATTTGAAGTCCCTGTGAATGGGCTTTTCTGAAAGGCAATTAAGAAATCCACTCAGAGAGGAC
TTGGGGTGAAACTTGGGTCCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCTTGCACACGC
TGTTGGCAAATGTCAGGACCAGGTTAAGTGAAGTGGCAGAAAACTTCCAGGTGGAACAAGCA
ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATC
CAGACTCCAGTTTCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT
TGCACCCTCCCCACCACACCCTGCACCAGACTGTACAGCCCAAGCCAGCAAGCACAGCCCT
GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGA
GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTACTGCGGGAGGATCAGC
TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAGGAACAGAGCCAGGGCAGGAGAGGTGGG
AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACGCTGGACCCAC
GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCCG
CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCAGCTCATCTCTG
TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC
CCAGGGCCTTCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAG
TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG
GCTGGGTGCCATCAGGGCCCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT
TCATGGATGCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCTCCTCAGCAGAATAGCT
GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA
TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAAC
CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG
GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
TCTTATGTGCTGCGAGGTGGTGAACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTG
GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCCAT
TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTTCGCATTGCTGAGACCTGGCTGGG
GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA
AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAGGAGACTGGGTGTGCGACATTCCACTGG
TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCCAGTTTCTCTGGAAA
GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT
GTCCCATGGTGTGGCTCCTTGACAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC
AGGAAGGAGATTCACTTTGGCAGCCACAGCACCTGTGCTTTGCTGTCAGGCAGGAGCAGGT
GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG
AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC
AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAGCCCGCCAGCAGTGGCGATTTGACCA
GATAAATGCTGTGGATGAACGATGATGTCAATGTCAGAAGGAAAAGAGAATTTTGGCCATC
AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT
GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT
TCACACCTTATTTTCATTGACTGCTGGCTGCTTA

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQNDQSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAKEKPCMERLQLQRRLGCRTFHWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEKDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQHWFQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACACAGCTGAGGAAGACCTCAGAC**ATGGA**
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC
 TGCCCCCTCCCACCGCCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACCAGCCCCAGCC
 CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCCCACGTATGTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGCGCAAGTCCTGCCTGGCACTG
 CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCCGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG
 ATTTCTGGACTATGGTTTTGACGCCCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGAGAGGGCACCTGCCACCCTGCGGCCATTC
 CTGTTGCGGGGGCGTGGGGAAGGTGTGGACCCCCAGCTCTATGTACAAATTACCATCTCCAT
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
 GACGCAGACCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCTTCGGGGACTCACCTACCCCCACCCC
 TGACCATGAGGAGCCCCGAGGGGGACCCCGGCCTGGGATGCCCCACCCCAAGGGGGCTCCAG
 CCTTCCAGTTGAACCGG**TGA**GGGCAGGGGCAATGGGATGGGAGGGCAAAGAGGGGAAGGCAAC
 TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC
 CTCCCACAGCCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCTTC
 CTTCTCCCAGTCTCTCAGGATCTGTGTCTTATTCTCTGCTGCCCATAACTCCAACCTCTGCCC
 TCTTTGGTTTTTTTCTCATGCCACCTTGTCTAAGACAACCTCTGCCCTCTTAACCTTGATTCCC
 CCTCTTTGTCTTGAACCTTCCCCCTTCTATTCTGGCCTACCCCTTGGTTCTTGACTGTGCCCTT
 TCCCTCTTCTCTCAGGATTCCCCTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGCAGCC
 AAGCAGGAGGCCAAGGGGGCCGGCACAGCCCCCATCCCCTGAGGGTGGGGCAGCTGTGGGGA
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCCCTTGACACACCACCCGGAACACTCCCCAGCC
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCCCTTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCAC
 AGGCCATTTGCACACGCTCCTGCACCCCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTCCTGCACACTTTACCTCTCATGTGCGTTTTCCCGGCCTGATGTTGTGGTGG
 TGTGCGGCGTGTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAGCCCCCTGC
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTGATGG
 TCTCGTCCCATTCCACACCATTTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA
 TCACCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA
 CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCCTGCTGCACTACATGAGAA
 AGGGACTCCCATTTGCCCTTCCCTTTCTCCTACAGTCCCTTTTGTCTTGTCTGTCCTGGCTG
 TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTTCCCAGCCT
 CCCTTTGGGCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC
 ATCGGGAGCTCTGCCTCCAAGTCTACCCTTCCCTTCCCGGACTCCCTCCTGTCCCCTCCTTT
 CCTCCCTCCTTCCCTTCCACTCTCCTTCCCTTTTGTCTCCCTGCCCTTTCCCCCTCCTCAGGTT
 CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCCCTCCTTCCCTTCTTCCCTGGCTCCTAGGCT
 GTGATATATATTTTTGTATTATCTCTTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTG
 GGATGTAAGTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

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FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGG**ATGG**
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACCAAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA
GGGGCCGCGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 206

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCCGTTGGTTGGTTGGTGCGGCTGAAGGGGTGTGGGCGGAGCAGCGTCGTTGGTTGGCCGGCGCG
CGGGCCGGGACGGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCGACTGGAGC
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCCTAAGTAGCCC
CCAGAGGCGCTGGGAGTGTTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGG
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCGAT
CGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACCTGCACAG
ACTCGCACGTCGCCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGAGGGGGGCTCCCCGCTTCCAC
CTGGCTGTCATCGGGTAGGGCGGGGCCGTGGGTTCAGGGGCGCACCACTTCCAAGCCTGTGT
CCCACAGGTCTTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAAC
TGGCACAAGTAAGTCCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCCTAGAGGGGCTCCCGA
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG
GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCC
ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC
ATGGAGGGGCTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGGCTAGGGGGTCTCT
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
CCTGGGACACACAGAGCCACCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC
ACGAGGGTGTCGTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT
GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCCACACTTGGCCAACCTGACCT
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC
GTGGGGGCGGAGACTCAGCTGGACAGCCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC
CTCAGGACCCCCCTCTCCGACCCCGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
GAGGGAATGGGGGTGGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGCGGGA
TGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 208

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP
```

Signal peptide:

amino acids 1-15

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FIGURE 209

AGCAGGAGCAGGAGAGGGACAATGGAAAGCTGCCCCGTCCAGGTTCATGTTCCCTCTTATTTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA
 TAGCATGGTGCAAAAATTCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACCTG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAATAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCCTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTTGACTTCTCCTTGGAACCTACATATGGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACCACACACACACACGACGTGCACACACGCACGCACGCGTGCACAC
 ACACACGCGCACACACACACACACACAGAGCTTCATTTCCCTGTCTTAAATCTCGTTTTCTC
 TTCTTCCTTCTTTTAAATTTATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCCCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCCCTGCTCTTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG
 ATGGTTTTTAAACACCTTTGTGAAATTGTCTTTTGGCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAACTCCATGCTTGGTTAGCATCTCCAACCTCCC
 TATGTAAATCAACAACCTGCATAATAAATAAAAGGCAATCATGTTATA

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLLFLLTCELAAEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRRLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMOVTEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQKGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
GACGCGGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATG**GCAGCGTCCGCCGGAGCCGGG
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTTCGGTGCTGGCGGCGGCGCTTGG
GCTCTTGACAGCTGGAGTATCAGCCTTGGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTC
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAG
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
TATATCTGTGATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTCTATAGAAGGAAA
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCCACCAGTTAAGCAGGC
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC
CTCAGCAAGAAACAAAACCAAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTC
AGGTCATTTACAATTGGGAGATTTAGAAAACATTCCTTTACCATCATTTAGAAATGGTTTG
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG
AAATGTGTCATATCAATTTCTGGATTACATAATAGCAAGATTAGCAAAGGATAAATGCCGAAG
GTCACCTTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTTGCTT
GAGAACTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTTA

FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASINIE
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCSSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTCAGCAGTGACTGCCCCGGGCTGCCGCC
CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC
TCTCGGCCACGGCTGGGTGCGGGGCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC
TGGCAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGCCCCCGACCCTGAGGCG
TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC
GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAGAAGTCT
TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCAGAAAAAGAA
TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGAATTTCG
TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT
ACTAAATTTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAACCTGGCAAGAA
AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAAT
CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
ACTTTTGGCTATAACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA
CTATATGCAGAAAAATTTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
TTAACACTATTTTATTAATTAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
CACATTTTGGGAGCTTTTCTACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACA
TGTTTATAAAGTAAAAAAA

FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
```

```
><subunit 1 of 1, 373 aa, 1 stop
```

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQ RAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTT RLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLT TVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
AGGCTGGTGGGAAGAAGCCGAG**ATG**GCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT
GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT
GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
GGAACCAGCAGGATGGTACCTTGTCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
TGGAGTCGCACCTGTCGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGGCCATGAGGTGGAGGACGTGGACCTGGA
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACACAGCCCCAGGCCCTGAGACGGCGG
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG
TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCCCTCATGATGTCAGG
AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
TTTGCTGTGTGCCACCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACATTGAAATGTG
TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTCAGAAACCCAAG
GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
TAAACTGTCCCCAGATCGACACGCAAAAAAAAA

FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPRRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELENTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWYIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGGSGLCVPPSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCCT
GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTCTGCCGGGGGCCACC
ATGCTGGTGA CTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC T
GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC
AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
TGGCCTTGCCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC
GCAAGAATTCTTGTGTCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAAC TCTCT
CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC
GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTCTGGACCGCCGC
GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGT CATCTTCATCTTTGTCTTCCT
CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTCTTCATGTTGACTTT
CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCCTTCATAGCCTTTCTACTTATTGAGT
TGGCTTGTGGATTATACTTTCCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA
GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTT CAGCATTTGCTCTG
CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCCTGGTAAGGCATGATGCT
GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
GACAAGATAGCTGGGACAGACTCTTGAATTCAGCTATCCGGGATTGTACAGATCTCTCTGT
GACTGACTTTGTGACTGTCCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCTCTGTGTTACTCCCATTTAGAAA
ATAAACACTTTTAAATGATCAAAAAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDIFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
VLLLGTLQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLEMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET
EQAGVLNWFVRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAVVGLEFTVVRHDA
ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATG**
 GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
 CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
 TGGT**TAGA**AAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
 CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
 AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCTCACTGACTTTTTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
```

```
><subunit 1 of 1, 188 aa, 1 stop
```

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ

IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIIISDNAVDNDSF

YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATC**ATG**GAACTTGCACTGCTGTGTGGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCCTGCGGACTAGGTGGCAG
AGGCCAACCCTAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCAC
TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACATTGTATGGAT
TTATCTCAACGCTATTGTTTAATGGCTGTGTTTAATGTGATCTATCTGGAAAATGAGGACTC
CGAA**TAA**AAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIPIQGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGLYKDNNKSSIHCMDSLQRYCLMAVFNVYILENEDSE
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACTCACCCGTGGGTCGCT**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAAA

FIGURE 224

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

Signal peptide:

amino acids 1-22

FOOTNOTES

FIGURE 225

GCTTGAGCGTGTGCGCGGTACACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
GAACTGGGTGCTCATCACGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT
TTTTTTTTTAACCGCCCCCTCCCCACCCCCCAAAAAAAGCTGTAAAGATGCAAAAACGTAATAT
CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
CCCAAGGGGTCCAATTTTTCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTC
ACAGGGGCTGTCATGCAACTGGCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA
CAATACAAAGGATGCGGTTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
TAGGTGTGAAGGCCAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA
TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT
CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
TGACGAAAATGCTTTTAATGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACCTTGGATCTGTCC
TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT
ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
TGGAACCTTTTGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGCG
ATGATCAGACTCAAAGAACTTCACCTGGAGCACAAATCAATTTTCCAAGCTCAACCTGGCCCT
TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGTATAG
GACAGACCATGTCTTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC
GAAGCTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA
TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGATATCCCTCAATGACA
TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTG
AAAAGTTTTAAAGGTCTAAGGGAGAAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT
TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCAGGCCGAAGCAT
GAGAGCAAACCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
TGACGCCGAGCACATCTCTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG
TGCTCGTCATCCTGCTGGTTATCTACGTGTCTATGGAAGCGGTACCCTGCGAGCATGAAGCAG
CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT
GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAAACCCACCACGAGACGAGCAGCGAGA
TGCTGTCTGAATGGGACGGGACCCCTGCACCTATAACAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTTAAAGCTGGAAATAAGTGGTGCTTTTATTGAACTC
TGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCCTTCCCTCTCCCTCTCACTTTGGTGG
CAAGATCCTTCCTTGTCCGTTTTAGTGCATTTCATAATACTGGTCATTTTCTCTCATACATA
ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAACCTCCGGTTTAATATAA
TACCTATTGTATAAGACCCCTTACTGATTCCATTAATGTGCGATTTGTTTTAAGATAAAACT
FCTTTTCATAGGTAAAAA

FIGURE 226

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301

><subunit 1 of 1, 513 aa, 1 stop

><MW: 58266, pI: 9.84, NX(S/T): 4

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQONLYLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKKRQSLKQMPSTQEFYVDYKPTNTTETSEMLLN
GTGPCTYNKSGSRECEV

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCTTT
TAAATATGTCAAGATCCAGACTTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
ATTGATTCTCACAGGCGACCATGGCAGTTTTTGTCTGTTGGAGACTTGGACTCTATTTATGG
GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
ATCCTGTTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
AAAACAACCTTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG
TTTAAATAGTAAAGTAGCAGGCTTTTGTATGTGTCACTGCTGTATCATACTTTTATGCTACAC
AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTTTCTCTGGAGCCTCAGGGCTTG
GCATTTATTGTCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
AAACATCAATAGATATCTAAAAA

VPAPCFGPLGSPPPYEEIVKTT

amino acids 1-29

amino acids 52-70

FIGURE 229

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA
 GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCC
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCCTTTAACT
 CCCTCTTCAAACCTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATAACAACCTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGC
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTTGCTTCTTCAGAAATGTTTTTTA
 CAATCTCAAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGATTTGGACTCATT
 TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAAAT
 GCTGTCCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
 CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCATGGAAC
 TCTAATTCTGTACATAAAAAATTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATG
 CTGTACTATGTCTTAAAGAGAATTTGGTAACTTGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTC
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTTGACAAGTGAAGAATGTTTAA
 TCATTCTGTCAATTTGTTCTCAATAGATGTAAGTGTAGACTACGGCTATTTGAAAAATGTG
 CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGA
 AGGTTAATTATTGTATATTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAATAGTT
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTTATGATGAGAGTAACAATA
 AAGTATTCATGATTTTTTACATACATGAATGTTTCATTTAAAAGTTTAATCCTTTGAGTGTCT
 ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTGAGGACTTTAGCCAGGTGTATATAATAAA
 GGTACTTTTGTGCTGCATTAAATTGCTTGGAAAGTGTTAACATTATATTATATAAGAGTATC
 CTTTATGAAATTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
 TTAAAAATAAGAACATTTAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAGCT
 GTATATAGCACAGGGAACCTAATCTTGGGTAATTCTAGTATAAAACAAATTATACTTTTAT
 TTAAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTCATAGTATTTTAT
 CTCTATAGTAAGTCTTAAGTGCAGCTAGCTTAGATTTAGACTATATAGAATTTAGATAT
 TGTATTGTTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAAAA
 TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTCTTCTCTCTGTA
 CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

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FIGURE 230

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR

Important features of the protein:**Signal peptide:**

amino acids 1-26

Protein: 15668

Variable	Mean	Standard deviation	Minimum	Maximum
Age	33.4	10.5	18	55
Gender	0.50	0.50	0	1
Marital status	0.50	0.50	0	1
Education	12.5	1.5	9	16
Income	1.5	0.5	1	2
Occupation	1.5	0.5	1	2
Religion	1.5	0.5	1	2
Political affiliation	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Subjective well-being	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	75.0	5.0	60	90
Health expectancy	60.0	5.0	45	75
Quality of life	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2

FIGURE 232

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></usr/seqdb2/sst/DNA/Dnasegs.min/ss.DNA77652
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><subunit 1 of 1, 353 aa, 1 stop
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><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLLAVSGAQTTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLGAGPYTTLAGLDLSHNLTSISPTAFSRLRYLESLLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPT I
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV
GODVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCTGTGGGTCTGAGG
GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA
AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT
GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC
GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCC
TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC
GGAAGATCAGCAGCCTCGCCAATTCCTTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTC
TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTTCGAGGT
CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCCAAACCACCATCTCTTTACT
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT
TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTTGTAATATCTT
TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGGCTATTTAATGTATTT
ATTTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
AGCAGGTGATGTATTTTTTATACAGTAAAAAAAAAAAAACCTTGTAATTCTAGAAGAGTGGCT
AGGGGGGTATTTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
TATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATT
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
CCAAAAAAAAAAAAAAAAAAAAA

FIGURE 234

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500

><subunit 1 of 1, 261 aa, 1 stop

><MW: 29667, pI: 8.76, NX(S/T): 0

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSTLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
CGAGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
TTACAGACACGTAGTGTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTG
TGTTTGGCAAAAAGTGAAGATGAGCATTATCCCCCTTGGAAATCAGTCATTGGAGGGATGATG
GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAAT
GGAAGGAAAAAGGAACTGGAAGGAAAACCATTCGATTTTCGTGGTGTACATCATGCATTTG
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAAACACTACTTGGT
ATTGAATACACCCTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACCATCTTGGCTGAGAATGACCC
CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
TTTTAA

Footnote 235

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA
RESAPYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEH
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHLYLVNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

239/249

FIGURE 237

CGGACGACGCTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
GCCTGAAGTCGGCGTGGGCGTTTGTAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
TTAAGAAGTAAAA**ATG**GCGAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTTACAGGC
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
TTCATTGGTTTTCATGTTGATGTTTGGGTCACCTATTGCTTCCATGTGGATTCTTTTTTGGTGC
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTTCAAATGCACTTA
TATTTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCT**TG**AGATCAC
TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT
ACACATTGCCAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTTATGTTT
TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTA
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTTATTCTGAGATTTAGAA
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAAGTAACCACTCTTGT
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG
CCGATTGCTTGAGGTCAAGTGTTTGTAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT
AAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCAGCTACCTGGGAGGC
TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTTCGCCAC
TGCACTCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
TAAAAGGTTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTTGGTAAAGA
AAAAATATTTGTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTTAAATGCCC
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVGILFFTGWIMIDAADVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIFGMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

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FIGURE 239

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGCCCGCAACACTCCGTCTCACCTCTGGGCCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT
 GGTCAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAG
GATGGAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTTTATTTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCAACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC
 AGCCAACTACTTTGCGTTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCCGGGGGGTGCCTGGTGCTGGTGG
 CCTCCTACGACGATCCAGGGACCAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTG
 GGGAGTTCCTACGCAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAAGCCCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTT**TAG**GGTGGC
 TGTGGCTCTTCCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCC
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCCTTGCACGC
 TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCCTCCCACAGCACATCCTACCCGGAAGACC
 AGCCTCAGAGGGTCCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTTCGTCAGGG
 ACTGCTGACGGCTGGTCCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA
 TTTTTGCTGGTTTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRLKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCC
 CTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTTGGCCA
 GCCTCTTACCCTGAGTGTGGAAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT
 GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC
 CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC
 CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT
 GTCTTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG
 AGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
 CCTTCTCCTGGCTGTTTATTTTCATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATTAAATTCCTTCTCAGATACCA
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCCTTCCCCTGGACATCTCTTAGAGAG
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGG
 GAAGTTTGGGATATACCCCAAAGTCCTCTACCCCTCACTTTTATGGCCCTTTCCTTAGATA
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATA
 TATTTGGAAATTAAAGTTTCTGACTTT

FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812

><subunit 1 of 1, 337 aa, 1 stop

><MW: 37668, pI: 6.27, NX(S/T): 1

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPA SYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT
LSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKS SVVFTSAQATTEA

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTC
GTGGACCCAAAGGTAGCAATCTGAAAC**ATG**AGGAGTACGATTCTACTGTTTTGTCTTCTAGG
ATCAACTCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTC
CGGATCAGGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTG
ATACCATTAACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG
AATGACACCTGGTACCCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAAC
TGCACCCACATGTGTTACCAATTTTTGTACACAACCTTGGAGCCCAGGGCACTATCCTAAGC
TCAGAGGAATTGCCACAAATCTTCAGAGCCTCATCATCCATTCCCTTGTTCCCGGGAGGCAT
CCTGCCCACCAGTCAGGCAGGGGCTAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAG
GAGCAGGTGTAAATCCTGCCACCCAGGGAACCCAGCAGGCCGCTCCCAACTCCCAGTGGC
ACAGATGACGACTTTGCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA
GGAAGCCACCACAGAATCAGCAAATGGAATTCAG**TAA**GCTGTTTCAAATTTTTTCAACTAAG
CTGCCTCGAATTTGGTGATACATGTGAATCTTTATCATTGATTATATTATGGAATAGATTGA
GACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATTTACCTGAAAATATTCTTGAAATT
TCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAACAATAATTCAATGGATAAAT
CTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTAAACATATTTGGAAA
ACTGGAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQOQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLSIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLLTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

2025-03-04 10:00:00

98

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG
GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCCTCCGCTCCAGCTCCGCGCTGCCCG
GCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCTCCCCGCAGCGGCTCCGCGGCCTCC
TGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAG
GAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT
TGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC
AATGGAGCTGAATGTTCAAGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAG
CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTGGCACTTGTTTCAGATTACCCAAAA
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATA
AATGCTTTAATTTTCATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGT
GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
TAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA
TAAAAGCTACCAATCTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAAT
AAAAATTATTTCCAACA

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIITYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

protein = 243 aa